

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 14:23:05 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-1

Perfect score: 18

Sequence: 1 tatcactoctggaagccc 18

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

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6: gb_pat.*

7: gb_ph.*

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13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

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28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	13.4	74.4	17	6	AX217324	AX217324	Sequence
2	13.4	74.4	17	6	AX217700	AX217700	Sequence
3	13.4	74.4	17	6	AX217701	AX217701	Sequence
c 4	13.2	73.3	31	6	AR084474	AR084474	Sequence
c 5	13.2	73.3	31	6	AR172373	AR172373	Sequence
6	12.8	71.1	20	6	AR126586	AR126586	Sequence
7	12.8	71.1	20	6	AR129611	AR129611	Sequence
8	12.8	71.1	20	6	AR162335	AR162335	Sequence
9	12.8	71.1	20	6	AR163817	AR163817	Sequence
10	12.8	71.1	20	6	AR172890	AR172890	Sequence
11	12.8	71.1	20	6	AR173817	AR173817	Sequence
12	12.8	71.1	20	6	AR174355	AR174355	Sequence
c 13	12.8	71.1	26	6	AR089898	AR089898	Sequence
c 14	12.6	70.0	31	6	AX249458	AX249458	Sequence
15	12.4	68.9	17	6	AX217699	AX217699	Sequence
16	12.4	68.9	17	6	AX218260	AX218260	Sequence
17	12.4	68.9	18	6	AR037237	AR037237	Sequence
18	12.4	68.9	18	6	AR048706	AR048706	Sequence
19	12.4	68.9	21	12	AB068713	AB068713	Synthetic
c 20	12.4	68.9	31	6	AX249305	AX249305	Sequence
c 21	12.4	68.9	45	6	AR033932	AR033932	Sequence
c 22	12.4	68.9	45	6	AR033936	AR033936	Sequence
c 23	12.4	68.9	45	6	AR175065	AR175065	Sequence
c 24	12.4	68.9	45	6	AR175069	AR175069	Sequence
c 25	12.4	68.9	45	6	AX032497	AX032497	Sequence
c 26	12.4	68.9	45	6	AX032505	AX032505	Sequence
c 27	12.2	67.8	20	6	AR117567	AR117567	Sequence
c 28	12.2	67.8	25	6	E37792	E37792	Isolation o
c 29	12.2	67.8	25	6	E46842	E46842	Isolation o
30	12.2	67.8	31	6	AR090082	AR090082	Sequence
c 31	12.2	67.8	46	6	AR032468	AR032468	Sequence
c 32	12.2	67.8	46	6	I29208	I29208	Sequence
c 33	12.2	67.8	46	6	I90882	I90882	Sequence
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35	12	66.7	30	6	AR118393	AR118393	Sequence
c 36	12	66.7	30	6	I43676	I43676	Sequence
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c 38	11.8	65.6	17	6	AX263256	AX263256	Sequence
c 39	11.8	65.6	17	6	AX263257	AX263257	Sequence
c 40	11.8	65.6	20	6	AR136235	AR136235	Sequence
c 41	11.8	65.6	20	6	AX201496	AX201496	Sequence
c 42	11.8	65.6	20	6	AX298295	AX298295	Sequence
c 43	11.8	65.6	24	6	I13144	I13144	Sequence
c 44	11.8	65.6	25	6	AR142911	AR142911	Sequence
c 45	11.8	65.6	25	6	AX035314	AX035314	Sequence

ALIGNMENTS

RESULT	1	AX217324	Sequence	2766	from Patent WO0159103.	17 bp	mRNA	linear	PAT 07-SEP-2001
LOCUS	AX217324	Sequence	2766	from Patent WO0159103.	17 bp	mRNA	linear	PAT 07-SEP-2001	
DEFINITION	AX217324	Sequence	2766	from Patent WO0159103.	17 bp	mRNA	linear	PAT 07-SEP-2001	
ACCESSION	AX217324	Sequence	2766	from Patent WO0159103.	17 bp	mRNA	linear	PAT 07-SEP-2001	
VERSION	AX217324.1	GI:15527385							
KEYWORDS		synthetic construct.							
SOURCE		synthetic construct.							
ORGANISM		artificial sequence.							
REFERENCE		1 (bases 1 to 17)							
AUTHORS		Blatt, L., Mcswigen, J. and Chowrira, B.M.							
TITLE		Method and reagent for the modulation and diagnosis of cd20 and							
JOURNAL		nogo gene expression							
		Patent: WO 0159103-A 2766 16-AUG-2001;							
		RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;							
		Mcswigen, James (US) ; Chowrira, Bharat M. (US)							
FEATURES		Location/Qualifiers							
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Query Match 74.4%; Score 13.4; DB 6; Length 17;
 Best Local Similarity 93.3%; Pred. No. 5.5e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
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 Db 3 ATCACTCCTGGCAGC 17

RESULT 2

AX217700 LOCUS AX217700 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 3142 from Patent WO0159103.
 ACCESSION AX217700
 VERSION AX217700.1 GI:15527761
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL Patent: WO 0159103-A 3142 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
 McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

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Query Match 74.4%; Score 13.4; DB 6; Length 17;
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 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
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 Db 2 ATCACTCCTGGCAGC 16

RESULT 3

AX217701 LOCUS AX217701 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 3143 from Patent WO0159103.
 ACCESSION AX217701
 VERSION AX217701.1 GI:15527762
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL Patent: WO 0159103-A 3143 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
 McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

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BASE COUNT 5 a 6 c 3 g 3 t
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 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4

AR084474/c LOCUS AR084474 31 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 10 from patent US 5981183.
 ACCESSION AR084474
 VERSION AR084474.1 GI:10011245
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)
 AUTHORS Takarada, Y., Inoue, H., Shibata, S. and Kawamura, Y.
 TITLE Method for amplifying and detecting of target nucleic acid sequence using thermostable enzyme
 JOURNAL Patent: US 5981183-A 10 09-NOV-1999;
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BASE COUNT 5 a 9 c 8 g 9 t
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 Db 27 TAGCACCCTATGGAAGCCC 10

RESULT 5

AR172373/c LOCUS AR172373 31 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 10 from patent US 6303306.
 ACCESSION AR172373
 VERSION AR172373.1 GI:17911864
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)
 AUTHORS Takarada, Y., Inoue, H., Shibata, S. and Kawamura, Y.
 TITLE Method for amplifying and detecting of target nucleic acid sequence using thermostable enzyme
 JOURNAL Patent: US 6303306-A 10 16-OCT-2001;
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QY 1 tatcactctctggaagccc 18
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 Db 27 TAGCACCCTATGGAAGCCC 10

RESULT 6

AR126586

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LOCUS       AR126586               20 bp    DNA
DEFINITION   Sequence 15 from patent US 6180353.
ACCESSION    AR126586
VERSION      AR126586.1  GI:14113179
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Dean,N.M. and Cowsert,L.M.
TITLE        Antisense modulation of daxx expression
JOURNAL      Patent: US 6180353-A 15 30-JAN-2001;
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RESULT 11
LOCUS ARI73817 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 15 from patent US 6306606.
ACCESSION ARI73817
VERSION ARI73817.1 GI:17914137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weber,M.J., Wyatt,J. and Cowser,L.M.
TITLE Antisense modulation of MP-1 expression
JOURNAL Patent: US 6306606-A 15 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 6 c 7 g 5 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcactctctggaagc 16
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Db 4 TCTCGCTCTCTGGAAGC 19

RESULT 12
LOCUS ARI74355 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 15 from patent US 6306655.
ACCESSION ARI74355
VERSION ARI74355.1 GI:17914675
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP alpha expression
JOURNAL Patent: US 6306655-A 15 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
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BASE COUNT 2 a 6 c 7 g 5 t
ORIGIN

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Best Local Similarity 87.5%; Pred. No. 1.3e+04;
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Db 4 TCTCGCTCTCTGGAAGC 19

RESULT 13
LOCUS AR089898/c 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 18 from patent US 5994076.
ACCESSION AR089898
VERSION AR089898.1 GI:10016653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL Patent: WO 0159103-A 3141 16-AUG-2001;
PITOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/db_xref="taxon:32630"

AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 18 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
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ORIGIN

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RESULT 14
LOCUS AX249458/c 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1537 from Patent WO0166800.
ACCESSION AX249458
VERSION AX249458.1 GI:15864081
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 31)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1537 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
source 1..31
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Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 25 TCACTCTCTGGAAG 13

RESULT 15
LOCUS AX217699 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 3141 from Patent WO0159103.
ACCESSION AX217699
VERSION AX217699.1 GI:15527760
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL Patent: WO 0159103-A 3141 16-AUG-2001;
PITOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
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BASE COUNT 3 a 6 c 5 g 3 t
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Db 4 ATCACTCCTGGCAG 17

Search completed: October 12, 2002, 16:51:10
Job time: 8885 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 14:25:35 ; Search time 792.17 Seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-1
Perfect score: 18
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Scoring table: IDENTITY_NUC
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	AA13829	Murine PDGFR-beta
2	13.8	76.7	50	AAL28262	Human SNP oligonuc
3	13.4	74.4	17	ABK02766	Human CD20 Hammerh
4	13.4	74.4	17	ABK03142	Human CD20 Inozyme
5	13.4	74.4	17	ABK03143	Human CD20 Inozyme
c 6	13.4	74.4	50	AAL33976	Human SNP oligonuc
c 7	13.2	73.3	31	AAQ92585	Thermus thermophil
c 8	13.2	73.3	31	AAQ92602	Thermus thermophil
9	13	72.2	28	AAZ88272	Granulocyte macrop

10	13	72.2	29	13	AAQ30835	Type III procollag
11	13	72.2	29	20	AAV83186	Primer for amplif
c 12	13	72.2	31	22	AAI31049	Human single nucle
13	12.8	71.1	20	22	AAS45602	Mouse GAPDH RT-PCR
14	12.8	71.1	20	22	AAS21535	Mouse GAPDH revers
15	12.8	71.1	20	22	AAS10515	Mouse GAPDH revers
16	12.8	71.1	20	22	AAH47971	Mouse GAPDH DNA pr
17	12.8	71.1	20	22	AAH12329	Mouse GAPDH DNA am
18	12.8	71.1	20	22	AAF62859	Mouse GAPDH revers
19	12.8	71.1	20	22	AAF72914	Mouse GAPDH PCR re
20	12.8	71.1	20	24	ABA03203	Mouse GAPDH quanti
21	12.8	71.1	20	24	ABA83456	Mouse GAPDH PCR pr
22	12.8	71.1	23	15	AAQ73528	Alpha-adducin cDNA
23	12.8	71.1	33	24	ABA96569	Human tyrosinase 9
c 24	12.8	71.1	41	22	AAH46672	Human NADH dehydro
c 25	12.8	71.1	42	22	AAH46670	Human NADH dehydro
c 26	12.8	71.1	50	22	AAI33581	Human SNP oligonuc
27	12.4	68.9	17	18	AAZ62339	Granule bound star
28	12.4	68.9	17	23	ABK03141	Human CD20 Inozyme
29	12.4	68.9	17	23	ABK03702	Human CD20 Anberzy
30	12.4	68.9	18	17	AAT36945	OVCAL gene exon 11
31	12.4	68.9	20	21	AAZ63828	Primer DAGKIAAfor
c 32	12.4	68.9	31	18	AAZ62577	Granule bound star
c 33	12.4	68.9	31	22	AAI30896	Human single nucle
c 34	12.4	68.9	45	18	AAT86960	DNA for soluble I-
c 35	12.4	68.9	45	18	AAT86952	DNA for soluble I-
c 36	12.4	68.9	47	21	AAZ69291	Human map-related
c 37	12.2	67.8	17	15	AAQ71843	Primer (RB-19) to
c 38	12.2	67.8	20	21	AAZ79534	Rat p38alpha antis
c 39	12.2	67.8	25	21	AAZ63818	Rhodobacter sphaer
c 40	12.2	67.8	25	21	AAZ51058	PCR primer-4 to am
c 41	12.2	67.8	25	21	AAZ46832	R. sphaeroides hyd
c 42	12.2	67.8	30	13	AAQ27061	HCV primer P32. S
c 43	12.2	67.8	46	15	AAQ69330	Human mast cell ch
c 44	12.2	67.8	46	18	AAT63792	Human mast cell ch
c 45	12.2	67.8	46	20	AAZ17080	Test sequence from

ALIGNMENTS

RESULT	1
AA13829	
ID	AA13829 standard; DNA; 18 BP.
XX	
AC	AA13829;
XX	
DF	27-JUL-2000 (first entry)
XX	
DE	Murine PDGFR-beta phosphorothioate antisense oligonucleotide SEQ ID NO:1.
XX	
KW	Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW	PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW	recurrent stenosis; cardiovascular injury; ss.
XX	
OS	Mus sp.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..18
FT	/*tag= a
XX	/note= "phosphorothioate linkages"
PN	CA2228977-A1.
XX	
PD	07-MAY-1999.
XX	
PF	03-FEB-1998; 98CA-2228977.
XX	
PR	07-NOV-1997; 97CA-2215360.
XX	
PA	(EDEL/) EDELMAN E R.
PA	(ROSE/) ROSENBERG R D.
PA	(SIRO/) SIROIS M G.

PA (SIMO/) SIMONS M.
 XX Edelman ER, Rosenberg RD, Sirolis MG, Simons M;
 XX WPI; 2000-283933/25.
 XX Antisense inhibition of platelet derived growth factor beta-receptor
 PT subunit expression for the prevention of restenosis -
 XX Claim 25; Page 15; 43pp; English.
 XX A method has been developed for preventing restenosis following vascular
 CC injury by antisense inhibition of platelet derived growth factor
 CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
 CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
 CC canal), especially of a valve in the heart, after surgical correction of
 CC the primary condition) following cardiovascular injury. The present
 CC sequence represents a phosphorothioate antisense oligonucleotide for
 CC murine PDGFR-beta.
 XX
 SQ Sequence 18 BP; 4 A; 7 C; 3 G; 4 T; 0 other;
 Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 7.2;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 taccactctggaagccc 18
 |||||
 Db 1 taccactctggaagccc 18
 RESULT 2
 AAL28262
 ID AAL28262 standard; DNA; 50 BP.
 XX
 AC AAL28262;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #1470.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX Claim 1; Page 1801; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 XX
 SQ Sequence 50 BP; 9 A; 19 C; 13 G; 9 T; 0 other;
 Query Match 76.7%; Score 13.8; DB 22; Length 50;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 atcactctggaagccc 18
 ||| |||||
 Db 12 atcgctctggaagtc 28
 ||| |||||
 RESULT 3
 ABK02766
 ID ABK02766 standard; RNA; 17 BP.
 XX
 AC ABK02766;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 Hammerhead ribozyme #55.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NCO; hammerhead ribozyme;
 KW DNase; inozyme; G-cleaver; amebzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 PR 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 XX

DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury -

XX Claim 30; Page 141; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NIGO).

CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky immunodeficiency virus associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-targetting nucleic acid is used to cleave RNA of the NIGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NIGO activity of the cell and treat a patient having a condition associated with the level of NIGO. The treatment may further comprise the use of one or more therapies. In particular, the NIGO-targetting nucleic acid may be used to treat stroke, Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NIGO expression. The present sequence is a hammerhead ribozyme of the invention.

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 U; 0 other;

Query Match 74.4%; Score 13.4; DB 23; Length 17;
 Best Local Similarity 73.3%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 atcaactcctggagc 16
 1:||||:|:|:|

Db 3 aacacuccggcgc 17

RESULT 4

ID ABK03142

XX ABK03142 standard; RNA; 17 BP.

AC ABR03142;

XX 12-MAR-2002 (first entry)

DE Human CD20 Inozyme #93.

XX Human; ss: antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme; DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04273.

XX 11-FEB-2000; 2000US-181797P.

PR 28-FEB-2000; 2000US-185516P.

PR 06-MAR-2000; 2000US-187128P.

XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.

PI Blatt L, McSwiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury -

XX Claim 30; Page 147; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NIGO).

CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky immunodeficiency virus associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-targetting nucleic acid is used to cleave RNA of the NIGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NIGO activity of the cell and treat a patient having a condition associated with the level of NIGO. The treatment may further comprise the use of one or more therapies. In particular, the NIGO-targetting nucleic acid may be used to treat stroke, Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NIGO expression. The present sequence is an inozyme of the invention.

XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 U; 0 other;

Query Match 74.4%; Score 13.4; DB 23; Length 17;
 Best Local Similarity 73.3%; Pred. No. 1.6e+03;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

XX SQ Sequence 50 BP; 13 A; 13 C; 13 G; 11 T; 0 other;

Query Match 74.4%; Score 13.4; DB 22; Length 50;
 Best Local Similarity 93.3%; Pred. No. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctggaagc 16
 | |||||
 DB 22 AACACTCTGGAAGC 8

RESULT 7
 AAQ92585/c
 ID AAQ92585 standard; DNA; 31 BP.

XX AC AAQ92585;
 XX DT 25-JAN-1996 (first entry)

XX DE Thermus thermophilus RNA polymerase promoter sequence #5 in PCR primer.
 XX KW Primer; promoter; PCR; amplification; reverse transcriptase;
 XX KW thermostable; polymerase; Vibrio; ribonuclease; ss.
 XX OS Synthetic.

XX PN WO9515399-Al.
 XX PD 08-JUN-1995.
 XX PF 01-DEC-1994; 94WO-JP02025.
 XX PR 01-DEC-1993; 93JP-0301823.
 XX PA (TOYM) TOYO BOSEKI KK.

XX PI Inoue H, Kawamura Y, Shibata S, Takarada Y;
 XX WPI; 1995-215277/28.

XX PT Amplification of poly:nucleotide(s) using thermostable enzymes -
 XX PT derived from Thermus thermophilus, allows reduction in non-specific
 XX PT hybridisation and high specificity.

XX PS Disclosure; Page 12; 59pp; Japanese.

XX CC A novel method is presented to amplify a target nucleic acid sequence
 CC which involves binding a mechanism similar to reverse transcriptase PCR
 CC in which a first primer is bound to a target RNA molecule and the first
 CC cDNA strand is synthesised with a thermostable RNA dependent DNA
 CC polymerase, the RNA strand is removed with a thermostable ribonuclease
 CC H, and the DNA strand is converted to a double stranded form by
 CC amplifying with a thermostable DNA polymerase from a second bound primer.
 CC The process differs by producing more copies of the target RNA strand
 CC with a DNA dependent RNA polymerase. The RNA polymerase primes from a
 CC promoter sequence, such as those shown in AAQ92581-Q92615, which is
 CC attached 5' of the target binding sequence of the first primer, e.g.

CC such as primers AAQ92576-80 for targeting the Vibrio TDH gene. The RNA
 CC produced is recycled back to the cDNA conversion step with the RNA
 CC dependent-DNA polymerase.

XX SQ Sequence 31 BP; 5 A; 9 C; 8 G; 9 T; 0 other;

Query Match 73.3%; Score 13.2; DB 16; Length 31;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcactctctggaagccc 18
 || ||| | |||||
 DB 27 TAGCACCCTGGAAGCCC 10

RESULT 8
 AAQ92602/c
 ID AAQ92602 standard; DNA; 31 BP.

XX AC AAQ92602;
 XX DT 25-JAN-1996 (first entry)

XX DE Thermus thermophilus RNA polymerase promoter sequence #22 in PCR primer.
 XX KW Primer; promoter; PCR; amplification; reverse transcriptase;
 XX KW thermostable; polymerase; Vibrio; ribonuclease; ss.

XX OS Synthetic.
 XX PN WO9515399-Al.
 XX PD 08-JUN-1995.

XX PF 01-DEC-1994; 94WO-JP02025.
 XX PR 01-DEC-1993; 93JP-0301823.
 XX PA (TOYM) TOYO BOSEKI KK.

XX PI Inoue H, Kawamura Y, Shibata S, Takarada Y;
 XX WPI; 1995-215277/28.

XX PT Amplification of poly:nucleotide(s) using thermostable enzymes -
 XX PT derived from Thermus thermophilus, allows reduction in non-specific
 XX PT hybridisation and high specificity.

XX PS Disclosure; Page 13; 59pp; Japanese.

XX CC A novel method is presented to amplify a target nucleic acid sequence
 CC which involves binding a mechanism similar to reverse transcriptase PCR
 CC in which a first primer is bound to a target RNA molecule and the first
 CC cDNA strand is synthesised with a thermostable RNA dependent DNA
 CC polymerase, the RNA strand is removed with a thermostable ribonuclease
 CC H, and the DNA strand is converted to a double stranded form by
 CC amplifying with a thermostable DNA polymerase from a second bound primer.
 CC The process differs by producing more copies of the target RNA strand
 CC with a DNA dependent RNA polymerase. The RNA polymerase primes from a
 CC promoter sequence, such as those shown in AAQ92581-Q92615, which is
 CC attached 5' of the target binding sequence of the first primer, e.g.
 CC such as primers AAQ92576-80 for targeting the Vibrio TDH gene. The RNA
 CC produced is recycled back to the cDNA conversion step with the RNA
 CC dependent-DNA polymerase.

XX SQ Sequence 31 BP; 5 A; 9 C; 8 G; 9 T; 0 other;

Query Match 73.3%; Score 13.2; DB 16; Length 31;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcactcctggaagccc 18
 || || | |||||
 Db 27 TAGCACCCTGGAAGCCC 10

RESULT 9

AAZ88272
 ID AAZ88272 standard; DNA; 28 BP.

XX
 AC AAZ88272;

XX
 DT 02-MAY-2000 (first entry)

XX
 DE Granulocyte macrophage colony stimulating factor PCR primer #2.

XX
 KW Sec B; granulocyte macrophage colony stimulating factor; GM-CSF;

XX
 KW protein secretion; PCR primer; ss.

XX
 OS Homo sapiens.

XX
 PN CN1236011-A.

XX
 PD 24-NOV-1999.

XX
 PF 15-MAY-1998; 98CN-0110840.

XX
 PR 15-MAY-1998; 98CN-0110840.

XX
 PA (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.

XX
 PI Gan R, Huang P, Qian Y;

XX
 DR WPI; 2000-148268/14.

XX
 PT Method for using molecule mate to promote protein secretion - using
 PT recombined expression carrier and prokaryote host cell

XX
 PS Example 2; Page 12; 29pp; Chinese.

XX
 CC The present invention uses the co-expression of molecule mate and
 CC required protein in prokaryotic cell, especially colon Bacillus host,
 CC to promote the secretion expression of required protein. Specifically,
 CC the present invention relates to recombined expression carrier for the
 CC required protein to secret and express in prokaryotic cell and the
 CC expression carrier contains the site after the gene sequence of
 CC encoding molecule mate is connected to the first promoter controllably.
 CC The encoding molecule mate gene sequence has a DNA sequence in the
 CC downstream to connect controllably the encoding required protein gene
 CC sequence to signal peptide containing the second promoter. The present
 CC sequence represents a PCR primer for a human granulocyte macrophage
 CC colony stimulating factor nucleotide sequence which is used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 28 BP; 6 A; 10 C; 5 G; 7 T; 0 other;

Query Match 72.2%; Score 13; DB 21; Length 28;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcactcctgga 13

|||||

Db 7 tatcactcctgga 19

RESULT 10

AAQ30835

ID AAQ30835 standard; cDNA; 29 BP.

XX
 AC AAQ30835;

XX
 DT 24-MAR-1993 (first entry)

XX

DE Type III procollagen primer III-2.

XX
 KW Mutation; pro-alpha(III); primer; PCR; ss.

XX
 OS Synthetic.

XX
 PN WO9219754-A.

XX
 PD 12-NOV-1992.

XX
 PF 08-MAY-1992; 92WO-US03866.

XX
 PR 08-MAY-1991; 91US-0696607.

XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.

XX
 PI Kuivaniemi SH, Prockop DJ, Tromp GC;

XX
 DR WPI; 1992-398878/48.

XX
 PT Kit for detecting genetic pre-disposition for vascular aneurysms
 PT - contains primer to amplify portions of Type III procollagen DNA
 PT and detects mutation in standard procollagen DNA

XX
 PS Disclosure; Page 12; 44pp; English.

XX
 CC Example 1 describes the determination of the presence of a mutation
 CC in the pro-alpha(III) gene. Primers used in PCR are given in
 CC AAQ30834-48.

XX
 SQ Sequence 29 BP; 5 A; 10 C; 7 G; 7 T; 0 other;

Query Match 72.2%; Score 13; DB 13; Length 29;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ctctctggaagccc 18

|||||

Db 11 ctctctggaagccc 23

RESULT 11

AAV83186

ID AAV83186 standard; DNA; 29 BP.

XX
 AC AAV83186;

XX
 DT 02-MAR-1999 (first entry)

XX
 DE Primer for amplifying GM-CSF cDNA.

XX
 KW Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
 KW immunomodulator; vector; vaccine; cancer; HIV; Leishmania;
 KW Mycobacterium; listeria; Plasmodium; retrovirus; evaluation;
 KW human immunodeficiency virus; PCR primer; ss.

XX
 OS Synthetic.

XX
 PN WO9844788-A2.

XX
 PD 15-OCT-1998.

XX
 PF 09-APR-1998; 98WO-US06944.

XX
 PR 09-DEC-1997; 97US-0069163.

XX
 PR 09-APR-1997; 97US-0838702.

XX
 PR 01-MAY-1997; 97US-0848760.

XX
 PA (CHAN/) CHANG L.

XX
 PI Chang L;

XX

DR WPI; 1999-024005/02.
 XX Use of immunodeficient mice comprising human cells - particularly
 PT SCID/beige mice comprising human immune cells for evaluating
 PT vaccines against cancers or human pathogens, e.g. HIV
 XX
 PS Example 1b; Page 36; 154pp; English.
 XX
 CC Immunodeficient mice comprising human cells can be used for
 CC exposure to human pathogens and/or their components or human
 CC tumour cells and human peripheral blood lymphocytes. Also claimed
 CC is a vaccine comprising a cell modified to express an antigen and
 CC an immune-modulating protein, this is preferably an expression
 CC vector comprising a polynucleotide sequence that encodes the
 CC antigen and immune-modulating protein. Such vectors can be used
 CC to treat a subject having a tumour by transferring the expression
 CC vector into the tumour so that the antigen and the immune-modulator
 CC are expressed by at least the tumour. The methods can be used for
 CC producing and evaluating vaccines including cancer vaccines and
 CC vaccines directed against human pathogens, e.g. HIV, Leishmania,
 CC Mycobacterium, Listeria or Plasmodium. This sequence is an
 CC intermediate retroviral vector derived from pLNL6, a vector approved
 CC for clinical use in the United States. pLNL6 is essentially pLNL6
 CC digested with ClaI and BclI to remove cloning sites and the pLNL6
 CC internal SmaI gene. These were replaced with a polylinker. A neo
 CC gene was then inserted under the transcriptional control of the SV40
 CC enhancer/promoter to create the vector pLSN. Two primers (AAV83185,
 CC AAV83186) were used to amplify the granulocyte macrophage colony
 CC stimulating factor (GM-CSF) cDNA (AAV83189) for lcs insertion into
 CC pLSN.
 XX
 SQ Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 other;

Query Match 72.2%; Score 13; DB 20; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcactcctgga 13
 |||||

Db 10 tatcactcctgga 22

RESULT 12
 AA131049/C
 ID AA131049 standard; DNA; 31 BP.
 XX
 AC AA131049;
 XX
 DT 18-OCT-2001 (first entry)
 XX
 DE Human single nucleotide polymorphism (SNP) MUT 2.
 XX
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KW single nucleotide polymorphism; SNP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(16,T)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200166800-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-US07268.
 XX
 PR 07-MAR-2000; 2000US-0187510.
 PR 22-MAY-2000; 2000US-0206129.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2001-522952/57.
 XX
 PT Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or
 PT severity of a particular phenotype or disorder (e.g. diabetes)
 PT associated with a particular genotype -
 XX
 PS Claim 1; Page 125; 145pp; English.
 XX
 CC The invention relates to the identification of nucleic acid molecules
 CC (AA129513-AA131314) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing.
 XX
 SQ Sequence 31 BP; 10 A; 7 C; 7 G; 7 T; 0 other;

Query Match 72.2%; Score 13; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 tcactcctggaag 15
 |||||

Db 25 TCACCTCCTGGAAG 13

RESULT 13
 AA545602
 ID AA545602 standard; DNA; 20 BP.

XX AC AA545602;

XX DT 18-DEC-2001 (first entry)

XX DE Mouse GAPDH RT-PCR reverse primer.

XX Human; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
 KW cytosolic; nontropic; neuroprotective; antiinflammatory; antidiabetic;
 KW immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
 KW oxidative stress; neurological disorder; parkinsonism; apoptosis;
 KW meningitis-associated intracranial complication; ischaemia; PCR primer;
 KW inflammatory disorder; autoimmune disorder; arthritis; diabetes;
 KW GAPDH; glyceraldehyde phosphate dehydrogenase.

XX OS Mus musculus.

XX PN WO200164955-A1.

XX PD 07-SEP-2001.

XX PF 01-MAR-2001; 2001WO-US06572.

XX PR 02-MAR-2000; 2000US-0517467.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Popoff I, Cowser LM;

XX DR WPI; 2001-602570/68.

XX Antisense compound useful for treating hyperproliferative,
 PT neurological, inflammatory and autoimmune disorders and diabetes
 PT inhibits human PARP -
 XX
 PS Example 13; Page 80; 168pp; English.

XX The invention relates to antisense oligonucleotides targeted to human
CC PARG nucleic acid and inhibiting expression of human PARG. PARG
CC (Poly (ADP-ribose) polymerase plays an important role in chromatin
CC decondensation, DNA replication, DNA repair, gene expression, malignant
CC transformation, cellular differentiation and apoptosis. The antisense
CC oligonucleotide inhibitors are useful for inhibiting the expression of
CC PARG in human cells or tissues. They are also useful for treating a
CC human with a disease associated with PARG especially hyperproliferative
CC disorders (e.g. cancer), cellular injury resulting from oxidative stress,
CC neurological (e.g. parkinsonism, meningitis-associated intracranial
CC complications and ischaemia), inflammatory and autoimmune disorders (e.g.
CC arthritis) and diabetes. The present sequence is an RT-PCR (reverse
CC transcriptase PCR) primer designed to amplify GAPDH (glyceraldehyde
CC phosphate dehydrogenase) as a control in an experiment to quantitate
CC PARG mRNA levels.
XX
SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 other;

Query Match 71.1%; Score 12.8; DB 22; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 14
AAS21535
ID AAS21535 standard; DNA; 20 BP.
XX
AC AAS21535;
XX
DT 21-NOV-2001 (first entry)
XX
DE Mouse GAPDH reverse PCR primer.
XX
KW Survivin; human; mouse; cytostatic; antisense oligonucleotide;
KW hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
XX
OS Mus musculus.
XX
PN WO200157059-A1.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US02939.
XX
PR 02-FEB-2000; 2000US-0496694.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Ackermann EU, Swayze EE, Cowdery LM;
XX WPI; 2001-488863/53.
XX
DR Novel antisense compounds for modulating the expression of Survivin and
PT treatment of cancer -
XX
PS Example 13; Page 51; 120pp; English.
XX
CC The invention relates to antisense oligonucleotides targeted to a nucleic
CC acid molecule encoding human Survivin, where the antisense
CC oligonucleotide inhibits the expression of human Survivin. These
CC antisense oligonucleotides are used in the treatment of an animal
CC suffering from a disease or condition associated with Survivin, e.g. a
CC hyperproliferative condition such as cancer, and comprises administering
CC a therapeutically or prophylactically effective amount of the antisense
CC oligonucleotide so that expression of Survivin is inhibited. The
CC oligonucleotides can also be used to treat a human suffering from a
CC disease or condition characterised by a reduction in apoptosis

CC comprising administering the antisense oligonucleotide to a human. In
CC addition, the antisense oligonucleotide and a cytotoxic chemotherapeutic
CC agent e.g. taxol or cisplatin, can be used to modulate apoptosis,
CC cytokinesis or the cell cycle, or inhibit the proliferation in a cancer
CC cell by contacting the cell with the antisense oligonucleotide.
CC AAS21531-AAS21768 represent Survivin nucleic acids, and antisense
CC oligonucleotides targeted to Survivin, used in the method of the
CC invention.
XX
SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 other;

Query Match 71.1%; Score 12.8; DB 22; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 15
AAS10515
ID AAS10515 standard; DNA; 20 BP.
XX
AC AAS10515;
XX
DT 24-OCT-2001 (first entry)
XX
DE Mouse GAPDH reverse PCR primer.
XX
KW Mouse; caspase 3; apoptosis; GAPDH; PCR primer; ss.
XX
OS Mus musculus.
XX
PN WO200153310-A1.
XX
PD 26-JUL-2001.
XX
PF 11-JAN-2001; 2001WO-US00888.
XX
PR 18-JAN-2000; 2000US-0484617.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Zhang H, Cowdery LM;
XX WPI; 2001-442252/47.
XX
PT New antisense compound to inhibit caspase 3 is useful for treating
PT hepatitis and atherosclerosis -
XX
PS Example 13; Page 81; 127pp; English.
XX
CC The present sequence for mouse GAPDH reverse PCR primer is used
CC with the forward PCR primer (AAS10514) to amplify DNA encoding
CC mouse GAPDH. The present sequence is described in an invention
CC relating to novel antisense oligonucleotides (AAS10517-AAS10676)
CC and methods of using these compounds for the modulation of caspase 3
CC expression. The caspase 3 antisense oligonucleotides specifically
CC hybridise with and inhibit the expression of caspase 3. Antisense
CC compounds targeted to caspase 3 are useful to inhibit caspase 3
CC expression in cells or tissues and to modulate apoptosis. The caspase 3
CC antisense oligonucleotides are useful for treating disorders associated
CC with expression of caspase 3. Such disorders include hyperproliferative
CC disorders (e.g. cancer), viral infections (e.g. hepatitis),
CC haematopoietic disorders, autoimmune disorders, atherosclerosis and
CC neurological disorders (e.g. Alzheimer's disease).
XX
SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 other;

Query Match 71.1%; Score 12.8; DB 22; Length 20;

Query Match

Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 tatcaactcctggaagc 16
| | | | | | | | | |
Db 4 tctcgcctcctggaagc 19

Search completed: October 12, 2002, 17:08:00
Job time: 9745 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 14:24:45 ; Search time 191.26 seconds
(without alignments) updates/sec
23.117 Million cell

Title: US-09-945-131-1

Perfect score: 18

Sequence: 1 tatcactctctggaagccc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	13.2	73.3	31	2	US-08-821-782-10
c 2	13.2	73.3	31	4	US-09-292-435A-10
3	13	72.2	29	4	US-08-848-760B-7
4	12.8	71.1	20	4	US-09-490-692-15
5	12.8	71.1	20	4	US-09-488-671-15
6	12.8	71.1	20	4	US-09-487-445-15
7	12.8	71.1	20	4	US-09-593-711A-15
8	12.8	71.1	20	4	US-09-484-617-15
9	12.8	71.1	20	4	US-09-721-822A-15
10	12.8	71.1	20	4	US-09-593-589-15
11	12.8	71.1	20	4	US-09-496-694B-15
12	12.8	71.1	26	2	US-08-859-998-18
13	12.8	71.1	26	4	US-09-235-928-18
14	12.4	68.9	17	4	US-08-679-645-214
15	12.4	68.9	18	1	US-08-399-986B-27
16	12.4	68.9	18	1	US-08-493-754A-27
17	12.4	68.9	31	4	US-08-679-645-452
c 18	12.4	68.9	45	2	US-08-596-387B-75
c 19	12.4	68.9	45	2	US-08-596-387B-83
c 20	12.4	68.9	45	4	US-09-067-615-75
c 21	12.4	68.9	45	4	US-09-067-615-83
c 22	12.4	68.9	45	5	PCT-US95-09816A-75
c 23	12.4	68.9	45	5	PCT-US95-09816A-83
c 24	12.2	67.8	40	3	US-09-286-904-58
25	12.2	67.8	31	2	US-08-859-998-202
26	12.2	67.8	31	4	US-09-225-928-202
c 27	12.2	67.8	46	1	US-08-171-389-80

c 28	12.2	67.8	46	1	US-08-123-936-80	Sequence 80, Appl
c 29	12.2	67.8	46	2	US-08-475-228A-80	Sequence 80, Appl
c 30	12.2	67.8	46	3	US-08-482-080A-80	Sequence 80, Appl
c 31	12.2	67.8	46	5	PCT-US93-12388-80	Sequence 80, Appl
32	12	66.7	30	1	US-08-154-019-10	Sequence 10, Appl
33	12	66.7	30	1	US-08-461-333-10	Sequence 10, Appl
34	12	66.7	30	3	US-08-464-167-10	Sequence 10, Appl
35	12	66.7	30	3	US-09-158-313-10	Sequence 10, Appl
36	12	66.7	30	3	US-08-476-798-10	Sequence 10, Appl
37	11.8	65.6	20	3	US-09-280-799-38	Sequence 38, Appl
c 38	11.8	65.6	24	1	US-08-158-682A-7	Sequence 7, Appl
39	11.8	65.6	25	4	US-08-928-465-7	Sequence 7, Appl
c 40	11.8	65.6	30	1	US-08-121-053-17	Sequence 17, Appl
c 41	11.8	65.6	30	1	US-08-455-063-17	Sequence 17, Appl
c 42	11.8	65.6	32	3	US-08-907-468-1	Sequence 1, Appl
c 43	11.8	65.6	37	4	US-09-481-288-12	Sequence 12, Appl
c 44	11.6	64.4	20	1	US-08-449-045C-32	Sequence 32, Appl
c 45	11.6	64.4	20	2	US-08-435-605A-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-821-782-10/c
; Sequence 10, Application US/08821782
; Patent No. 5981183
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 61601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Dos 5.0
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ahern, Paul L.
; REGISTRATION NUMBER: 17020
; REFERENCE/DOCKET NUMBER: 66425
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: (25)3533
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-08-821-782-10

APPLICANT: Chang, Lung-Ji
 TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: United States of America
 ZIP: 32606

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:

NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
8-760B-7

Match	72.2%; Score
Local Similarity	100.0%; pre
S 13; Conservative	0; M
1 tatcactcctgga 13	
0 TATCACTCCTGGA 22	

4
0-692-15
Page 15, Application US/09490692
No. 6180353
L INFORMATION:
AGENT: Nicholas M. Dean
CANT: Lex M. Cowsett

REFERENCE: RTS-0120
 NNT APPLICATION NUMBER: US/09/490,692
 NNT FILING DATE: 2000-01-24
 R OF SEQ ID NOS: 176

NO 13
TH: 20
: DNA
NISM: Artificial Sequence

PCR INFORMATION: PCR FAILURE
00-692-15

Match	71.18;
Local Similarity	87.58;

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 5

US-09-488-671-15
; Sequence 15, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
; APPLICANT: Robert Mckay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt.
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
; FILE REFERENCE: RTS-0123
; CURRENT APPLICATION NUMBER: US/09/488,671A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-488-671-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 6

US-09-487-445-15
; Sequence 15, Application US/09487445
; Patent No. 6258600
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
; FILE REFERENCE: RTS-0107
; CURRENT APPLICATION NUMBER: US/09/487,445
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-487-445-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 7

US-09-593-711A-15
; Sequence 15, Application US/09593711A
; Patent No. 6271030

; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-593-711A-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 8

US-09-484-617-15
; Sequence 15, Application US/09484617
; Patent No. 6303374
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
; FILE REFERENCE: RTS-0103
; CURRENT APPLICATION NUMBER: US/09/484,617
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-484-617-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctctggaagc 16
| | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 9

US-09-721-822A-15
; Sequence 15, Application US/09721822A
; Patent No. 6306606
; GENERAL INFORMATION:
; APPLICANT: Michael J. Weber
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF MP-1 EXPRESSION
; FILE REFERENCE: RTS-0142
; CURRENT APPLICATION NUMBER: US/09/721,822A
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-721-822A-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 10
US-09-593-589-15
; Sequence 15, Application US/09593589
; Patent No. 6306655
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP ALPHA EXPRESSION
; FILE REFERENCE: RTS-0119
; CURRENT APPLICATION NUMBER: US/09/593,589
; CURRENT FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-593-589-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 11
US-09-496-694B-15
; Sequence 15, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-496-694B-15

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 4 tctcgctctctggaagc 19

RESULT 12
US-08-859-998-18/c
; Sequence 18, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-18

Query Match 71.1%; Score 12.8; DB 2; Length 26;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactctctggaagc 16
| | | | | | | | | | | | | | | |
Db 22 TATGACACCTGGAAGC 7

RESULT 13
US-09-225-928-18/c
; Sequence 18, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex

Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-225-928-18

Query Match 71.1%; Score 12.8; DB 4; Length 26;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcactctctggaagc 16
||| || |||||
Db 22 TATGACACCTGGAAGC 7

RESULT 14
US-08-679-645-214
; Sequence 214, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-214

Query Match 68.9%; Score 12.4; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 atcactctctggaag 15
|:|:|:|:|
Db 3 AUCUCUCCUGGAAG 16

RESULT 15
US-08-399-986B-27
; Sequence 27, Application US/08399986B
; Patent No. 5801041
; GENERAL INFORMATION:
; APPLICANT: Godwin, Andrew K.
; TITLE OF INVENTION: No. 5801041el Gene Associated with Suppression
; TITLE OF INVENTION: of Tumor Development
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,986B
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

; NAME: Hagan, Patrick J.
; REGISTRATION NUMBER: 27,643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-399-986B-27

Query Match 68.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactcctggaagc 16
|| |||||
Db 5 TCCCTCTCTGGAAGC 18

Search completed: October 12, 2002, 16:54:34
Job time: 8989 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:09:10 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-1

Perfect score: 18

Sequence: 1 tatcactctctggaagccc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	16	US-09-241-561-1	Sequence 1, Appli
2	15.4	85.6	25	35	US-09-954-427-302324	Sequence 302324,
3	15.4	85.6	25	62	US-60-233-166-302324	Sequence 302324,
4	14.8	82.2	25	74	US-60-353-987-128993	Sequence 128993,
5	14.4	80.0	25	17	US-09-396-196F-69450	Sequence 69450, A
6	14.4	80.0	25	17	US-09-396-196F-69451	Sequence 69451, A
c 7	13.8	76.7	25	35	US-09-954-427-98726	Sequence 98726, A
8	13.8	76.7	25	35	US-09-954-427-253488	Sequence 253488,
c 9	13.8	76.7	25	62	US-60-233-166-98726	Sequence 98726, A
10	13.8	76.7	25	62	US-60-233-166-253488	Sequence 253488,
c 11	13.8	76.7	25	74	US-60-353-987-358641	Sequence 358641,
c 12	13.8	76.7	25	74	US-60-353-987-614848	Sequence 614848,
13	13.4	74.4	25	26	US-09-660-220-110931	Sequence 110931,
c 14	13.4	74.4	25	35	US-09-954-427-162374	Sequence 162374,
c 15	13.4	74.4	25	35	US-09-954-427-162386	Sequence 162386,
c 16	13.4	74.4	25	35	US-09-956-584-185260	Sequence 185260,
17	13.4	74.4	25	35	US-09-956-584-318707	Sequence 318707,
c 18	13.4	74.4	25	35	US-09-956-584-362472	Sequence 362472,
c 19	13.4	74.4	25	62	US-60-233-166-162374	Sequence 162374,
c 20	13.4	74.4	25	62	US-60-233-166-162386	Sequence 162386,
c 21	13.4	74.4	25	62	US-60-234-017-153617	Sequence 153617,
c 22	13.4	74.4	25	62	US-60-234-017-280338	Sequence 280338,
c 23	13.4	74.4	25	62	US-60-234-017-355634	Sequence 355634,
24	13.2	73.3	25	26	US-09-660-220-66859	Sequence 66859, A
25	13.2	73.3	25	26	US-09-660-247-719	Sequence 719, App
26	13.2	73.3	25	26	US-09-660-247-723	Sequence 723, App
c 27	13.2	73.3	25	35	US-09-954-427-349744	Sequence 349744,
28	13.2	73.3	25	35	US-09-956-584-88931	Sequence 88931, A
c 29	13.2	73.3	25	35	US-09-956-584-122601	Sequence 122601,
30	13.2	73.3	25	62	US-60-232-638-876	Sequence 876, App
31	13.2	73.3	25	62	US-60-232-638-887	Sequence 887, App

US-09-396-196F-69450
; Sequence 69450, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-69450

Query Match 80.0%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactcctggaagccc 18
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Db 4 tcactcctggaagccc 19

RESULT 6
US-09-396-196F-69451
; Sequence 69451, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-69451

Query Match 80.0%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactcctggaagccc 18
||||| |||||||
Db 1 tcactcctggaagccc 16

RESULT 7
US-09-954-427-98726/c
; Sequence 98726, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427

; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98726
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA858718
US-09-954-427-98726

Query Match 76.7%; Score 13.8; DB 35; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactcctggaagccc 17
||||| |||||||
Db 22 TATCACCCTGGAAGCC 6

RESULT 8
US-09-954-427-253488
; Sequence 253488, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI044232
US-09-954-427-253488

Query Match 76.7%; Score 13.8; DB 35; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcactcctggaagccc 18
||||| |||||||
Db 1 atcactcctggaagccc 17

RESULT 9
US-60-233-166-98726/c
; Sequence 98726, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98726
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA858718
US-60-233-166-98726

Query Match 76.7%; Score 13.8; DB 62; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctggaagcc 17
||||| | |||||
DB 22 TATCACCCTGGAAGCC 6

RESULT 10

US-60-233-166-253488
; Sequence 253488, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 2000-10-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AI044232
US-60-233-166-253488

Query Match 76.7%; Score 13.8; DB 62; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcactctggaagcc 18
||||| | |||||
DB 1 atcactctggaagctc 17

RESULT 11

US-60-353-987-358641/c
; Sequence 358641, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 358641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-358641

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcactctggaagcc 18
||||| | |||||
DB 22 ATCACTCTGGTGCC 6

RESULT 12

US-60-353-987-614848/c
; Sequence 614848, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 614848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-614848

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcactctggaagcc 17
||||| | |||||
DB 17 TGTCACTCTCTGGAATCC 1

RESULT 13

US-09-660-220-110931
; Sequence 110931, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: US/09/660,220
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110931
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X03066
US-09-660-220-110931

Query Match 74.4%; Score 13.4; DB 26; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctggaagc 16
||||| | |||||
DB 7 atcactctggaatc 21

RESULT 14

US-09-954-427-162374/c
; Sequence 162374, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162374
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA925104

US-09-954-427-162374

Query Match 74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 cactctggaagccc 18
|||||
Db 19 CACTCTGGAGACC 5

RESULT 15

US-09-954-427-162386/c
; Sequence 162386, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mitmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162386
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA925104
US-09-954-427-162386

Query Match 74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 cactctggaagccc 18
|||||
Db 22 CACTCTGGAGACC 8

Search completed: October 12, 2002, 20:42:28
Job time: 16398 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 14:27:25 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-1
Perfect score: 18
Sequence: 1 tatcactctctggaagccc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/pct_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	18	100.0	18	5	US-09-945-131-1		Sequence 1, Appli
2	14.4	80.0	25	5	US-09-396-196G-69450		Sequence 69450, A
3	14.4	80.0	25	5	US-09-396-196G-69451		Sequence 69451, A
4	13.4	74.4	17	5	US-09-780-164-65		Sequence 65, Appl
5	13.4	74.4	17	5	US-09-780-164-441		Sequence 441, App
6	13.4	74.4	17	5	US-09-780-164-442		Sequence 442, App
7	13.2	73.3	25	6	US-10-215-112-2937		Sequence 2937, Ap
8	13.2	73.3	25	6	US-10-215-112-7753		Sequence 7753, Ap
9	13	72.2	25	5	US-09-396-196G-41662		Sequence 41662, A
10	13	72.2	25	5	US-09-396-196G-41663		Sequence 41663, A
11	13	72.2	25	5	US-09-396-196G-41664		Sequence 41664, A
12	12.8	71.1	20	1	PCT-US02-22672-15		Sequence 15, Appl
13	12.8	71.1	20	5	US-09-666-269B-8		Sequence 8, Appli
14	12.8	71.1	20	6	US-10-181-107-15		Sequence 15, Appl
15	12.8	71.1	20	6	US-10-181-177-15		Sequence 15, Appl
16	12.8	71.1	20	6	US-10-181-316-15		Sequence 15, Appl
17	12.8	71.1	20	6	US-10-181-542-15		Sequence 15, Appl
18	12.8	71.1	20	6	US-10-181-846-15		Sequence 15, Appl
19	12.8	71.1	20	6	US-10-182-049-15		Sequence 15, Appl
20	12.8	71.1	23	6	US-10-188-777-6		Sequence 6, Appli
21	12.8	71.1	25	5	US-09-396-196G-56409		Sequence 56409, A
22	12.8	71.1	25	5	US-09-396-196G-56426		Sequence 56426, A
23	12.8	71.1	25	5	US-09-396-196G-80096		Sequence 80096, A
24	12.8	71.1	26	5	US-09-225-201B-18		Sequence 18, Appl
25	12.4	68.9	17	5	US-09-780-164-440		Sequence 440, App

26 12.4 68.9 17 5 US-09-780-164-1001 Sequence 1001, Ap
27 12.4 68.9 25 5 US-09-956-604-57406 Sequence 57406, A
28 12.4 68.9 25 5 US-09-956-604-57407 Sequence 57407, A
29 12.4 68.9 25 5 US-09-956-604-57408 Sequence 57408, A
30 12.4 68.9 25 5 US-09-956-604-57415 Sequence 57415, A
31 12.4 68.9 25 5 US-09-956-604-57434 Sequence 57434, A
32 12.4 68.9 25 5 US-09-956-604-57436 Sequence 57436, A
33 12.4 68.9 25 5 US-09-956-604-57440 Sequence 57440, A
34 12.4 68.9 25 5 US-09-956-604-57441 Sequence 57441, A
35 12.4 68.9 25 5 US-09-956-604-57442 Sequence 57442, A
36 12.4 68.9 25 5 US-09-956-604-57443 Sequence 57443, A
c 37 12.4 68.9 25 5 US-09-956-604-57475 Sequence 57475, A
c 38 12.4 68.9 25 5 US-09-956-604-57476 Sequence 57476, A
c 39 12.4 68.9 25 5 US-09-956-604-57478 Sequence 57478, A
c 40 12.4 68.9 25 5 US-09-956-604-57479 Sequence 57479, A
c 41 12.4 68.9 25 5 US-09-956-604-57481 Sequence 57481, A
c 42 12.4 68.9 25 5 US-09-956-604-57482 Sequence 57482, A
c 43 12.4 68.9 25 5 US-09-956-604-57485 Sequence 57485, A
c 44 12.4 68.9 25 5 US-09-396-196G-37587 Sequence 37587, A
45 12.4 68.9 25 5 US-09-396-196G-37588 Sequence 37588, A

ALIGNMENTS

RESULT 1
US-09-945-131-1
; Sequence 1, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-1

Query Match 100.0% Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcactctctggaagccc 18
Db 1 tatcactctctggaagccc 18

RESULT 2
US-09-396-196G-69450
; Sequence 69450, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mitmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

```
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-69450

Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactctctggaagccc 18
   ||||| |||||
Db 4 tcactctctggaagccc 19

RESULT 3
US-09-396-196G-69451
; Sequence 69451, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-69451

Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tcactctctggaagccc 18
   ||||| |||||
Db 1 tcactctctggaagccc 16

RESULT 4
US-09-780-164-65
; Sequence 65, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-65

Query Match      74.4%; Score 13.4; DB 5; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.7e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
   |:|:|:|:|:|:|
Db 3 acaacuccuggcagc 17

RESULT 5
US-09-780-164-441
; Sequence 441, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 441
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-441

Query Match      74.4%; Score 13.4; DB 5; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.7e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
   |:|:|:|:|:|:|
Db 2 acaacuccuggcagc 16

RESULT 6
US-09-780-164-442
; Sequence 442, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 442
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-442

Query Match      74.4%; Score 13.4; DB 5; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.7e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 atcactctctggaagc 16
   |:|:|:|:|:|:|
Db 1 acaacuccuggcagc 15
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; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41662
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41662

Query Match          72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcaactctctgga 13
   ||||| |||||
Db 11 tatcaactctctgga 23

RESULT 10
US-09-396-196G-41663
; Sequence 41663, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41663
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41663

Query Match          72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcaactctctgga 13
   ||||| |||||
Db 8 tatcaactctctgga 20

RESULT 11
US-09-396-196G-41664
; Sequence 41664, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41664

US-10-215-112-2937
; Sequence 2937, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2937

Query Match          73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcaactctctggaagccc 18
   ||||| ||||| |||||
Db 5 tatcaactctctggaagctc 22

RESULT 8
US-10-215-112-7753
; Sequence 7753, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-7753

Query Match          73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcaactctctggaagccc 18
   ||||| ||||| |||||
Db 1 tatcaactctctggaagctc 18

RESULT 9
US-09-396-196G-41662
; Sequence 41662, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
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US-09-396-196G-41664

Query Match 72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcaactcctgga 13
| | | | | | | | | |
Db 2 tatcaactcctgga 14

RESULT 12
PCT-US02-22672-15
; Sequence 15, Application PC/TUS0222672
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Madeline M. Butler
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
; FILE REFERENCE: ISPH-0693
; CURRENT APPLICATION NUMBER: PCT/US02/22672
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/915,814
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
PCT-US02-22672-15

Query Match 71.1%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctgga 16
| | | | | | | | | |
Db 4 tctcgctcctgga 19

RESULT 13
US-09-666-269B-8
; Sequence 8, Application US/09666269B
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: C. Frank Bennett
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; APPLICANT: William Ricketts
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF FLIP-C EXPRESSION
; FILE REFERENCE: RTS-0202
; CURRENT APPLICATION NUMBER: US/09/666,269B
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 133
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-666-269B-8

Query Match 71.1%; Score 12.8; DB 5; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctgga 16
| | | | | | | | | |
Db 4 tctcgctcctgga 19

RESULT 14
US-10-181-107-15
; Sequence 15, Application US/10181107
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
; FILE REFERENCE: RTSP-0325
; CURRENT APPLICATION NUMBER: US/10/181,107
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: PCT/US01/00888
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 09/484,617
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-181-107-15

Query Match 71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctgga 16
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Db 4 tctcgctcctgga 19

RESULT 15
US-10-181-177-15
; Sequence 15, Application US/10181177
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
; FILE REFERENCE: RTSP-0334
; CURRENT APPLICATION NUMBER: US/10/181,177
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/00955
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 09/487,445
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-181-177-15

Query Match 71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcaactcctgga 16
| | | | | | | | | |
Db 4 tctcgctcctgga 19

Search completed: October 12, 2002, 17:27:27
Job time: 10802 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:10 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18
Sequence: 1 tctgagcactaaagctgg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	12.4	68.9	27	6	AX116019	AX116019 Sequence
c 5	12.2	67.8	21	6	AX353507	AX353507 Sequence
c 6	12	66.7	39	6	AX207258	AX207258 Sequence
c 7	11.8	65.6	20	6	AX175139	AX175139 Sequence
c 8	11.8	65.6	20	6	AX175147	AX175147 Sequence
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10	11.8	65.6	32	6	E14820	E14820 PCR primer
11	11.8	65.6	33	6	AX168196	AX168196 Sequence
c 12	11.8	65.6	34	6	A40268	A40268 Sequence 8
c 13	11.8	65.6	45	6	A11864	A11864 Nucleotide
c 14	11.8	65.6	48	9	HSB010889	AJ010889 Homo sapi
c 15	11.8	65.6	50	9	AF057502	AF057502 Homo sapi
c 16	11.6	64.4	24	6	AX138596	AX138596 Sequence
c 17	11.6	64.4	26	6	AX049166	AX049166 Sequence
c 18	11.6	64.4	26	6	AX049771	AX049771 Sequence
c 19	11.6	64.4	26	6	AX050769	AX050769 Sequence
c 20	11.6	64.4	27	6	A50992	A50992 Sequence 33
c 21	11.6	64.4	30	6	AR021104	AR021104 Sequence
c 22	11.6	64.4	33	6	A77273	A77273 Sequence 61
c 23	11.6	64.4	34	23	E11247	E11247 PCR primer
c 24	11.6	64.4	35	6	AX001436	AX001436 Sequence
c 25	11.6	64.4	42	10	MMU299488	AJ299488 Mus muscu
c 26	11.4	63.3	22	6	I81225	I81225 Sequence 9
c 27	11.4	63.3	24	6	AX104235	AX104235 Sequence
c 28	11.4	63.3	24	6	AX262438	AX262438 Sequence
c 29	11.4	63.3	24	6	AX355033	AX355033 Sequence
c 30	11.4	63.3	25	6	A22036	A22036 Oligonucleo
c 31	11.4	63.3	27	9	S81137	S81137 T cell anti
c 32	11.4	63.3	41	6	AX184259	AX184259 Sequence
c 33	11.4	63.3	50	6	AX157550	AX157550 Sequence
c 34	11.2	62.2	21	6	AR031042	AR031042 Sequence
c 35	11.2	62.2	21	6	AX097000	AX097000 Sequence
c 36	11.2	62.2	21	6	AX191211	AX191211 Sequence
c 37	11.2	62.2	21	12	AB069060	AB069060 Synthetic
c 38	11.2	62.2	24	6	AX117122	AX117122 Sequence
c 39	11.2	62.2	25	6	A35701	A35701 Mutated HRV
c 40	11.2	62.2	25	6	AR109013	AR109013 Sequence
c 41	11.2	62.2	25	6	I05539	I05539 Sequence 5
c 42	11.2	62.2	25	6	I06065	I06065 Sequence 12
c 43	11.2	62.2	26	6	A34026	A34026 Synthetic P
c 44	11.2	62.2	26	6	A34027	A34027 Synthetic P
c 45	11.2	62.2	26	6	A77247	A77247 Sequence 35

ALIGNMENTS

RESULT 1	AX079136	AX079136	19 bp	DNA	linear	PAT 22-FEB-2001
LOCUS	Sequence 16 from Patent WO0106004.					
DEFINITION	AX079136					
ACCESSION	AX079136.1	GI:13158709				
VERSION						
KEYWORDS	synthetic construct.					
SOURCE	synthetic construct.					
ORGANISM	artificial sequence.					
REFERENCE	1 (bases 1 to 19)					
AUTHORS	Richardson, P. and Cox, P.					
TITLE	A method for amplifying low abundance nucleic acid sequences and means for performing said method					
JOURNAL	Patent: WO 0106004-A 16 25-JAN-2001;					
FEATURES	CAMBRIDGE UNIVERSITY TECHNICAL SERVICES LIMITED (GB)					
source	Location/Qualifiers					
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
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Db 1 TCTGACCAACAAGCTGG 18

RESULT 2
LOCUS AX196752 24 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 459 from Patent WO0151627.
ACCESSION AX196752
VERSION AX196752.1 GI:15386958
KEYWORDS soybean.
SOURCE Glycine max
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
TITLE Nucleic acid molecules and other molecules associated with soybean
JOURNAL cyst nematode resistance
PATENT: WO 0151627-A 459 19-JUL-2001;
MONSANTO COMPANY (US)
FEATURES
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Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
    ||||| || ||||| |||
Db 1 TCTGACCAACAAGCTGG 18

RESULT 3
LOCUS AX196754 24 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 461 from Patent WO0151627.
ACCESSION AX196754
VERSION AX196754.1 GI:15386960
KEYWORDS soybean.
SOURCE Glycine max
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
TITLE Nucleic acid molecules and other molecules associated with soybean
JOURNAL cyst nematode resistance
PATENT: WO 0151627-A 461 19-JUL-2001;
MONSANTO COMPANY (US)
FEATURES
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ORIGIN

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Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
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Db 1 TCTGACCAACAAGCTGG 18

RESULT 4
LOCUS AX116019 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1142 from Patent WO0129262.
ACCESSION AX116019
VERSION AX116019.1 GI:14032961
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1142 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
    Location/Qualifiers
        1..27
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Best Local Similarity 92.9%; Pred. No. 4.2e+04;
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Db 26 TCTGACACTAAG 13

RESULT 5
LOCUS AX353507/c 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 39 from Patent WO0204636.
ACCESSION AX353507
VERSION AX353507.1 GI:18618582
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS van Roy,F., Goossens,S., Janssens,B. and Vanpoucke,G.
TITLE Novel _g(a) expressed in heart and testis
JOURNAL Patent: WO 0204636-A 39 17-JAN-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
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            /db_xref="taxon:9606"
            /note="splice acceptor 16"
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
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Db 10 CTGAGCACTGAAGCT 24

RESULT 10
LOCUS E14820 32 bp DNA linear PAT 28-JUL-1999
DEFINITION PCR primer for gaining rabbit M-CSF gene.
ACCESSION E14820
VERSION E14820.1 GI:5709503
KEYWORDS JP 1998014581-A/4.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Matsuyama,K., Ota,A., Kato,K. and Shimamura,S.
TITLE RABBIT-TYPE MACROPHAGE COLONY STIMULANT FACTOR AND DNA FRAGMENT
CODING THE SAME
JOURNAL Patent: JP 1998014581-A 4 20-JAN-1998;
MORINAGA MILK IND CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1998014581-A/4
PD 20-JAN-1998
PF 08-JUL-1996 JP 1996177916
PI MATSUYAMA KOKI, OTA ATSUSHI, KATO KAYOKO, SHIMAMURA SEIICHI PC
(C12N15/09,C07K14/535,C12N1/21,C12P21/02,C12N1/21,C12R1:19), PC
(C12P21/02,
PC C12R1:19);
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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FH Location/Qualifiers
FT source 1..32
Location/Qualifiers
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctgagcactaaagc 15
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Db 17 TCTGAGCACTGCAGC 31

RESULT 11
LOCUS AX168196 33 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 36 from Patent WO0142474.
ACCESSION AX168196
VERSION AX168196.1 GI:14597469
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 33)
AUTHORS Welcher,A., Wen,D. and Kelly,M.
TITLE Interferon-like molecules and uses thereof
JOURNAL Patent: WO 0142474-A 36 14-JUN-2001;
Angen Inc. (US)
FEATURES
Location/Qualifiers

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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgagcactaaagctg 17
    ||||| ||||| |||||
Db 14 TGAGCACCACCTG 28

RESULT 12
LOCUS A40268/c 34 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 8 from Patent WO9424300.
ACCESSION A40268
VERSION A40268.1 GI:2296364
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 34)
AUTHORS Jacobs,E.
TITLE TRANSPOSITION ASSEMBLY FOR GENE TRANSFER IN EUKARYOTES
JOURNAL TRANSGENE SA (FR)
Patent: WO 9424300-A 8 27-OCT-1994;
COMMENT Other publication AU 6571994 941108
Other publication FR 2703996 941021
Other publication CA 2160697 941027.
FEATURES
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Location/Qualifiers
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
    ||||| ||||| |||||
Db 21 CAGAGCACTGAAGCT 7

RESULT 13
LOCUS All1864 45 bp mRNA linear PAT 10-JAN-1994
DEFINITION Nucleotide sequence 12 from patent number EP0387775.
ACCESSION All1864
VERSION All1864.1 GI:492543
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Beug,H., Birnstiel,M.L., Cotten,M., Wagner,E. and Kandolf,H.
TITLE Genetic construct for inhibiting RNA function
JOURNAL Patent: EP 0387775-A 12 19-SEP-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H.
FEATURES
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/db_xref="taxon:32644"
BASE COUNT 17 a 9 c 10 g 9 t
ORIGIN

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 Best Local Similarity 86.7%; Pred. No. 8.9e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tgcagcactaaagctg 17
 |||| || |||||
 Db 25 TGAGGACCAAGCTG 39

RESULT 14

HSA010889

LOCUS

DEFINITION HSA010889 48 bp mRNA linear PRI 02-MAR-1999
 donor 009 haplotype, A2 A3 B7 B37.

ACCESSION

AJ010889

VERSION AJ010889.1 GI:3559912

KEYWORDS beta-chain; T-cell receptor; VDJC region.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission

Submitted (04-SEP-1998)

University of Cambridge Clinical School, Level 5 Box 157,

Addenbrooke's Hospital, Hills Road, Cambridge, CB2 2QQ, UK

2 (bases 1 to 48)

Weekes,M.P., Wills,M.R., Mynard,K., Carmichael,A.J. and

Sissons,J.G.

The memory cytotoxic T-lymphocyte (CTL) response to human

cytomegalovirus infection contains individual peptide-specific CTL

clones that have undergone extensive expansion in vivo

J. Virol. 73 (3), 2099-2108 (1999)

99138992

FEATURES

Location/Qualifiers

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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 25 CTGAACACTGAAGCT 39

RESULT 15

AF057502/c

LOCUS

DEFINITION AF057502 50 bp DNA linear PRI 01-AUG-1999

Homo sapiens clone C53B Smu-Sgamma4 immunoglobulin switch

recombination junction.

ACCESSION

AF057502

VERSION AF057502.1 GI:5668863

KEYWORDS

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

Pan,Q., Rabbani,H. and Hammarstrom,L.

Characterization of human gamma 4 switch region polymorphisms

suggests a meiotic recombinational hot spot within the Ig locus:

influence of S region length on IgG4 production

J. Immunol. 161 (7), 3520-3526 (1998)

98430672

MEDLINE

REFERENCE

Pan,Q. and Hammarstrom,L.

Direct Submission

Submitted (06-APR-1998)

Clinical Immunology, Karolinska Institute,

Huddinge Hospital, Huddinge S141-86, Sweden

Location/Qualifiers

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BASE COUNT

ORIGIN

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Best Local Similarity

Matches 13; Conservative

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Db 27 TCTGAGCTCCAAAGC 13

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Job time: 8888 sec

65.6%; Score 11.8; DB 9; Length 50;

Best Local Similarity 86.7%; Pred. No. 8.8e+04;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:00 ; Search time 792.17 seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	13.2	73.3	19	AAZ89251	Rat adenosine rece
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4	13.2	73.3	21	AAZ74041	Human biallelic ma
5	13.2	73.3	24	AAI61828	Soybean 240017 reg
6	13.2	73.3	24	AAI61830	Soybean 240017 reg
c 7	13	72.2	41	AAZ48359	Primer specific fo
c 8	12.8	71.1	47	AAAT03932	Factor-V NASBA pri
9	12.4	68.9	18	AAZ74877	Human biallelic ma

c	10	12.4	68.9	27	22	AAH38346	SNP specific lower
c	11	12.2	67.8	27	18	AAZ72197	Mouse flk-1 VEGF r
c	12	12.2	67.8	30	20	AAZ12424	PCR primer used to
c	13	12.2	67.8	30	21	AAZ55464	Neisseria species
c	14	12.2	67.8	38	16	AAQ92440	TCR gamma constant
c	15	12	66.7	39	22	AAH43130	Primer: F5-alpha-t
c	16	11.8	65.6	20	22	AAQ08118	Murine chordin-lik
c	17	11.8	65.6	20	22	AAQ08126	Murine chordin-lik
c	18	11.8	65.6	21	21	AAA36864	MM/LGMD2B region p
c	19	11.8	65.6	21	21	AAA11409	Human dysferlin PC
c	20	11.8	65.6	24	21	AAQ01967	Antisense PCR prim
c	21	11.8	65.6	26	22	AAH75969	Human interferon-1
c	22	11.8	65.6	27	13	AAQ25386	PCR primer D for r
c	23	11.8	65.6	28	21	AAZ59472	Poliovirus Sabin s
c	24	11.8	65.6	32	19	AAV12748	Primer for rabbit
c	25	11.8	65.6	33	22	AAQ08270	Human interferon-L
c	26	11.8	65.6	34	15	AAQ73086	5' primer to ampli
c	27	11.8	65.6	36	20	AAZ08584	Anti-EGFP hammehe
c	28	11.8	65.6	36	20	AAZ78668	Anti-green fluorese
c	29	11.8	65.6	38	21	AAZ60588	PCR primer used to
c	30	11.8	65.6	38	22	AAZ72336	5' PCR Primer used
c	31	11.8	65.6	50	21	AAZ48337	Primer specific fo
c	32	11.6	64.4	24	22	AAZ48337	Human G-CSF forwar
c	33	11.6	64.4	26	22	AAZ48337	Primer specific fo
c	34	11.6	64.4	26	22	AAZ48337	Primer #5 used to
c	35	11.6	64.4	26	22	AAZ48337	Human homolog of D
c	36	11.6	64.4	26	22	AAZ48337	Human homolog of D
c	37	11.6	64.4	27	17	AAZ48337	Interleukin-2 gene
c	38	11.6	64.4	30	14	AAQ37676	Human stem cell fa
c	39	11.6	64.4	34	17	AAA40130	Probe complementar
c	40	11.6	64.4	35	20	AAZ22453	Human IL-8 recepto
c	41	11.6	64.4	38	22	AAZ22453	Human CPRM1 DNA ex
c	42	11.6	64.4	41	20	AAZ19292	Polyoma virus vpl
c	43	11.6	64.4	47	21	AAZ68517	Human granulocyte
c	44	11.4	63.3	18	22	AAQ09707	Human map-related
c	45	11.4	63.3	20	20	AAZ99938	Cryptosporidium pa
							PCR primer used to

ALIGNMENTS

RESULT	1
AAAL3830	
ID	AAAL3830 standard; DNA; 18 BP.
XX	
AC	AAAL3830;
XX	
DT	27-JUL-2000 (first entry)
XX	
DE	Murine PDGFR-beta phosphorothioate antisense oligonucleotide SEQ ID NO:2.
XX	
KW	Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW	PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW	recurrent stenosis; cardiovascular injury; ss.
XX	
OS	Mus sp.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..18
FT	/*tag= a
XX	/note= "phosphorothioate linkages"
PN	CA2228977-A1.
XX	
PD	07-MAY-1999.
XX	
PF	03-FEB-1998; 98CA-2228977.
XX	
PR	07-NOV-1997; 97CA-2215360.
XX	
PA	(EDEL/) EDELMAN E R.
PA	(ROSE/) ROSENBERG R D.
PA	(SIRO/) SIROIS M G.

PA (SIMO/) SIMONS M.
XX Edelman ER, Rosenberg RD, Sirols MG, Simons M;
PI
XX
DR WPI; 2000-283933/25.
XX
PT Antisense inhibition of platelet derived growth factor beta-receptor
PT subunit expression for the prevention of restenosis -
XX
XX
PS Claim 25; Page 15; 43pp; English.
XX
CC A method has been developed for preventing restenosis following vascular
CC injury by antisense inhibition of platelet derived growth factor
CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
CC canal), especially of a valve in the heart, after surgical correction of
CC the primary condition) following cardiovascular injury. The present
CC sequence represents a phosphorothioate antisense oligonucleotide for
CC murine PDGFR-beta.
XX
SQ Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
|||||
DB 1 tctgagcactaaagctgg 18

RESULT 2
AAZ89251
ID AAZ89251 standard; DNA; 19 BP.
XX
AC AAZ89251;
XX
XX 09-JUN-2000 (first entry)
DT
XX
DE Rat adenosine receptor 2a forward PCR primer.
XX
KW Rat; expression profile; Three Prime End Amplification; TPEA;
KW adenosine receptor 2a; PCR primer; ss.
XX
OS Rattus sp.
XX
XX WO200008208-A2.
PN
XX
PD 17-FEB-2000.
XX
XX
XX 05-AUG-1999; 99WO-GB02579.
PF
XX
XX 05-AUG-1998; 98GB-0017055.
PR
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
XX Freeman TC, Richardson PJ, Dixon AK;
PI
XX
XX WPI; 2000-224033/19.
DR
XX
XX Reverse transcription of mRNA species used for expression profiling of
PT single cells by employing a first healed primer to provide first strand
PT cDNA species and then a second healed primer population to generate
PT second strand cDNAs -
XX
XX Example 1; Page 30; 50pp; English.
PS
XX This invention describes a novel process (M1) of reverse transcribing
CC mRNA species present in a sample from an organism by: (a) reverse
CC transcribing the mRNA species using a first healed primer, to provide a
CC first strand cDNA species; and (b) synthesizing second cDNA species
CC using a second healed primer population, the nucleotide sequences of the

CC non-heel portions of the second healed primers being such that the
CC reverse transcribed first strand cDNA species are capable of hybridizing
CC to at least one second primer. The processes can be used for expression
CC profiling of single cells. The polynucleotide comprising an oligo d(T)
CC sequence and a heel sequence 5' can be used for the reverse
CC transcription of mRNA species in a sample. The polynucleotide primer
CC population of claim (4) can be used for the synthesis of second strand
CC cDNA from a population of first strand cDNA species. Single cell cDNA
CC libraries can be made for subsequent detailed analysis of gene expression
CC and the discovery of novel genes. Small samples can be used and allow
CC the utilization of the large amount of sequence data available for
CC further understanding of disease processes and the cellular physiology of
CC complex issues. The invention provides a rapid, robust and reproducible
CC procedure called Three Prime End Amplification (TPEA), optionally with
CC PCR (TPEA-PCR). Prior art methods for the analysis of gene expression
CC within single cells or small tissue samples are limiting. Whilst in situ
CC hybridization techniques provide detailed information about the
CC cellular expression pattern of a gene in intact tissue the technique is
CC laborious and unable to analyze multiple transcripts in a single
CC preparation. The methods presented in the disclosure provide a more
CC straightforward, reproducible and reliable cDNA amplification procedure
CC for small mRNA samples where expression profiling can be conducted. The
CC amplification technique can be carried out in a single tube with a need
CC for only limited manual intervention and large numbers of samples can
CC be analyzed. There is a bias towards more uniform length cDNA molecules
CC ensuring that even relatively low abundance mRNA species are transcribed
CC and optionally amplified at the same level of efficiency as more
CC abundant mRNA species. AAZ89191-Z89253 represent the primers described in
CC the method of the invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;

Query Match 73.3%; Score 13.2; DB 21; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
|||||
DB 1 tctgaccacaagaagctgg 18

RESULT 3
AAZ57945
ID AAF57945 standard; DNA; 19 BP.
XX
XX AAF57945;
XX
XX 20-APR-2001 (first entry)
DT
XX
XX Low abundance nucleic acid amplification PCR primer #16.
DE
XX Nucleic acid amplification; low abundance sequence; expression profiling;
KW high throughput analysis; PCR primer; ss.
KW
XX Synthetic.
XX
XX WO200106004-A2.
PN
XX
XX 25-JAN-2001.
PD
XX
XX 19-JUL-2000; 2000WO-EP06887.
PF
XX
XX 19-JUL-1999; 99US-0144666.
PR
XX
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES.
PA
XX Richardson P, Cox P;
PI
XX WPI; 2001-138470/14.
DR
XX
XX Increasing the number of nucleotide sequences for low quantity mRNA
PT species from a sample for detection and cloning of gene sequences -

XX PS Example 1; Page 110; 120pp; English.

CC CC The present invention describes methods of increasing the number of

CC CC nucleic acid sequences corresponding to an mRNA present in a sample using

CC CC heeled primer sequences in amplification reactions. This is useful in the

CC CC detection and cloning of low copy number mRNAs in a sample, in expression

CC CC profiling and in high throughput systems.

XX SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;

Query Match 73.3%; Score 13.2; DB 22; Length 19;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18

Db 1 tctgaccacaaagctgg 18

RESULT 4

AAZ74041

ID AAZ74041 standard; DNA; 21 BP.

XX AC AAZ74041;

XX DT 10-SEP-2001 (first entry)

XX DE Human biallelic marker downstream amplification primer SEQ ID NO:8397.

XX KW Human genome; biallelic marker; high density disequilibrium map;

XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX KW haplotyping; hybridisation; identification; characterisation;

XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;

XX KW diagnosis; ss.

XX OS Homo sapiens.

XX PN WO9954500-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 99WO-IB00822.

XX PR 21-APR-1998; 98US-0082614.

XX PR 23-NOV-1998; 98US-0109732.

XX PA (GBST) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI; 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium

XX PT map of the human genome

XX PS Claim 8; Page 2021; 2745pp; English.

XX AA265654 to AA269578 represent human biallelic markers from the present

CC CC invention, which contain a polymorphic base at position 24 of their

CC CC nucleotide sequences. AA269579 to AA277440 represent amplification

CC CC primers for the biallelic markers. The biallelic markers of the

CC CC invention have a variety of uses: they can be used for high density

CC CC mapping of the human genome, and in complex association studies and

CC CC haplotyping studies which are useful in determining the genetic basis

CC CC for disease states. Compositions and methods of the invention can also

CC CC be useful for the identification of the targets for the development of

CC CC pharmaceutical agents and diagnostic methods, as well as the

CC CC characterisation of the differential efficacious responses to and side

CC CC effects from pharmaceutical agents acting on a disease as well as other

CC CC treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297

CC and 3367, are not actually given a sequence in the Sequence Listing

CC from the present invention.

XX SQ Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 other;

Query Match 73.3%; Score 13.2; DB 21; Length 21;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18

Db 2 tatgagcaccacaaagctgg 19

RESULT 5

AAI61828

ID AAI61828 standard; DNA; 24 BP.

XX AC AAI61828;

XX DT 16-OCT-2001 (first entry)

XX DE Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 459.

XX KW Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;

XX KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;

XX KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer; ss.

XX OS Glycine max.

XX PN WO200151627-A2.

XX PD 19-JUL-2001.

XX PF 05-JAN-2001; 2001WO-US00552.

XX PR 07-JAN-2000; 2000US-0174880.

XX PA (MONS) MONSANTO CO.

XX PI Hauge BM, Wang ML, Parsons JD, Parnell LD;

XX DR WPI; 2001-425872/45.

XX PT New purified nucleic acid for producing a soybean plant having soybean

XX PT cyst nematode resistance and for use in plant breeding programs -

XX PS Claim 25; Page 1149; 1353pp; English.

XX CC The invention relates to nucleic acid molecules from regions of the

CC CC soybean genome which are associated with soybean cyst nematode (SCN)

CC CC resistance. The nucleic acids are used to transform plants, and can

CC CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.

CC CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes

CC CC of soybean plants and for introgressing SCN resistance or partial SCN

CC CC resistance into soybean plants. They can also be used in plant breeding

CC CC programmes. The invention also relates to proteins encoded by such

CC CC nucleic acid molecules, as well as antibodies capable of recognising

CC CC these proteins. The present sequence is a primer used to amplify a

XX CC region of the soybean genome.

XX SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 other;

Query Match 73.3%; Score 13.2; DB 22; Length 24;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18

Db 2 tatgaccacacaaagctgg 19

```
RESULT 6
AAI61830
ID AAI61830 standard; DNA; 24 BP.
XX
XX AAI61830;
XX
XX 16-OCT-2001 (first entry)
XX
XX Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 461.
DE
XX
KW Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;
KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer; ss.
XX
XX Glycine max.
OS
XX
XX WO200151627-A2.
FN
XX
XX 19-JUL-2001.
PD
XX
XX 05-JAN-2001; 2001WO-US00552.
XX
XX 07-JAN-2000; 2000US-0174880.
PR
XX
XX (MONS ) MONSANTO CO.
PA
XX
XX Hauge BM, Wang ML, Parsons JD, Parnell LD;
PI
XX
XX WPI; 2001-425872/45.
DR
XX
XX New purified nucleic acid for producing a soybean plant having soybean
XX cyst nematode resistance and for use in plant breeding programs .
PT
XX
XX Claim 25; Page 1149; 1353pp; English.
PS
XX
XX The invention relates to nucleic acid molecules from regions of the
CC soybean genome which are associated with soybean cyst nematode (SCN)
CC resistance. The nucleic acids are used to transform plants, and can
CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.
CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes
CC of soybean plants and for introgressing SCN resistance or partial SCN
CC resistance into soybean plants. They can also be used in plant breeding
CC programmes. The invention also relates to proteins encoded by such
CC nucleic acid molecules, as well as antibodies capable of recognising
CC these proteins. The present sequence is a primer used to amplify a
CC region of the soybean genome.
XX
XX Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 other;
SQ

Query Match 73.3%; Score 13.2; DB 22; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
Db 2 tatgaaccctaaagctgg 19

RESULT 7
AAZ48359/c
ID AAZ48359 standard; DNA; 41 BP.
XX
XX AAZ48359;
AC
XX
XX 27-MAR-2000 (first entry)
DT
XX
XX Primer specific for Giardia sp giardin.
DE
XX
XX Microorganism; virus; polymerase chain reaction; food; cosmetic;
KW clinical diagnostic; molecular beacon; PCR primer; ss.
XX
```

```
OS Giardia sp.
XX
XX WO9631112-A2.
PN
XX
XX 09-DEC-1999.
PD
XX
XX 18-MAY-1999; 99WO-US10940.
XX
XX 18-MAY-1998; 98US-0086025.
PR
XX 17-MAY-1999; 99US-0086025.
XX
XX (HUNT-) HUNT WESSON INC.
PA
XX
XX Romick TL, Fraser MS;
PI
XX
XX WPI; 2000-086985/07.
DR
XX
XX Detection of microorganisms and viruses, for use in the food and
XX cosmetic industries and for clinical diagnostics .
PT
XX
XX Disclosure; Page 19; 63pp; English.
PS
XX
XX The invention provides a novel in vitro method for the detection of
CC microorganisms and viruses. The method comprises: (1) forming a
CC polymerase chain reaction (PCR) mixture by combining a predetermined
CC volume of a sample to be tested for the presence of a nucleic acid
CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
CC comprising 5'-GCTAAGGTCCTCAAGT-3', and a second primer comprising
CC 5'-AGACGCTCTCTACC-3', and PCR reagents; (2) forming a PCR product by
CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
CC to replicate and attain 0.25-1000mug nucleotide product/mul mixture; (3)
CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTCTAAGCCACC-3', to
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
CC the nucleic acid sequence, if present, and change the conformation of the
CC probe; and (4) determining whether or not bacteria are present in the
CC sample by detecting the conformational change of the probe, a
CC conformational change indicating the presence of bacteria in the sample.
CC The methods can be used for the detection of viruses and microorganisms,
CC including bacteria, yeast, molds and protista. They can be used in the
CC food and cosmetic industry and in clinical diagnostics. Using the method
CC it is not necessary to remove non-hybridized probe from the system.
XX
XX Sequence 41 BP; 10 A; 9 C; 11 G; 11 T; 0 other;
SQ

Query Match 72.2%; Score 13; DB 21; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 agcactaaagctg 17
Db 28 AGCACTAAGCTG 16

RESULT 8
AAT03932/c
ID AAT03932 standard; DNA; 47 BP.
XX
XX AAT03932;
AC
XX
XX 20-DEC-1995 (first entry)
DT
XX
XX Factor-V NASBA primer P1.
DE
XX
XX Factor-V; thrombosis; thrombophilia; diagnosis; anticoagulant;
KW activated protein-C; APC; homozygosity; heterozygosity;
KW primer; nucleic acid sequence based amplification; NASBA; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1..27
FT /*tag= a
```



```

FT XX /function= T7 RNAP promoter sequence
PN XX W09521938-A1.
XX XX
PD XX 17-AUG-1995.
XX XX
PF XX 14-FEB-1995; 95WO-EP00553.
XX XX
PR XX 14-FEB-1994; 94EP-0200377.
XX XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX XX
PI Bertina RM, Reitsma PH;
XX XX
DR WPI; 1995-293134/38.
XX XX
PT Screening for genetic defect associated with thrombosis and/or poor
PT anticoagulant response to activated protein C - useful to determine
PT homozygosity or heterozygosity for a mutation in Factor V, Va, VIII
PT or VIIa.
XX XX
PS Example 3; Page 46; 98pp; English.
XX XX
CC The amplification primers and detection probes given in AAT03932-38
CC are used for NASBA of human Factor-V DNA in order to detect a
CC mutation at codon 506 associated with an increased risk of
CC thrombotic events. Primer P1 is located in exon 10 of the
CC Factor V coding sequence.
XX XX
SQ Sequence 47 BP; 13 A; 10 C; 8 G; 16 T; 0 other;

Query Match 71.1%; Score 12.8; DB 16; Length 47;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tgagcactaaagctgg 18
Db 47 TCAGAACAAAGCTGG 32

RESULT 9
AAZ74877
ID AAZ74877 standard; DNA; 18 BP.
AC AAZ74877;
XX XX
DT 10-SEP-2001 (first entry)
XX XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:9233.
XX XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX XX
OS Homo sapiens.
XX XX
PN W09954500-A2.
XX XX
PD 28-OCT-1999.
XX XX
PF 21-APR-1999; 99WO-IB00822.
XX XX
PR 21-APR-1998; 98US-0082614.
XX XX
PR 23-NOV-1998; 98US-0109732.
XX XX
PA (GEST ) GENSET.
XX XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX XX
DR WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX Claim 8; Page 2199; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX XX
SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 other;

Query Match 68.9%; Score 12.4; DB 21; Length 18;
Best Local Similarity 92.9%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 agcactaaagctgg 18
Db 2 agcactgaagctgg 15

RESULT 10
AAH38346/c
ID AAH38346 standard; DNA; 27 BP.
XX XX
AC AAH38346;
XX XX
DT 14-AUG-2001 (first entry)
XX XX
DE SNP specific lower PCR primer SEQ ID 1142.
XX XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX XX
OS Homo sapiens.
XX XX
PN WO200129262-A2.
XX XX
PD 26-APR-2001.
XX XX
PF 13-OCT-2000; 2000WO-US28436.
XX XX
PR 15-OCT-1999; 99US-0160096.
XX XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX XX
PI Picoult-Newburg L, Pohl M;
XX XX
DR WPI; 2001-290930/30.
XX XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX XX
PS Claim 1; Page 55; 83pp; English.

```

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence.

XX
 SQ Sequence 27 BP; 9 A; 5 C; 6 G; 7 T; 0 other;

Query Match 68.9%; Score 12.4; DB 22; Length 27;
 Best Local Similarity 92.9%; Pred. No. 3e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 13; Conservative 0;

QY 1 tctgagcactaaag 14
 ||||| |||||
 Db 26 TCTGACACTAAG 13

RESULT 11

AAAX72197
 ID AAX72197 standard; RNA; 27 BP.
 XX
 AC AAX72197;
 XX
 XX 28-JUL-1999 (first entry)
 DT
 XX
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme #441.
 XX
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 XX Synthetic.
 OS Mus sp.
 XX
 XX WO9715662-A2.
 PN
 XX
 XX 01-MAY-1997.
 PD
 XX
 XX 25-OCT-1996; 96WO-US17480.
 PF
 XX
 XX 11-JAN-1996; 96US-0584040.
 PR 26-OCT-1995; 95US-0005974.
 XX
 XX (CHIR) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 PI WPI; 1997-259017/23.
 DR
 XX
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or

PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 XX psoriasis, rheumatoid arthritis, etc., in a human patient
 XX Claim 9; Page 136; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 SQ Sequence 27 BP; 9 A; 6 C; 7 G; 4 U; 1 other;

Query Match 67.8%; Score 12.2; DB 18; Length 27;
 Best Local Similarity 61.1%; Pred. No. 3.9e+03;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
 :|:| | |||||:
 Db 8 ucugaugangaaagcugg 25

RESULT 12
 AAX12424/C
 ID AAX12424 standard; DNA; 30 BP.
 XX
 AC AAX12424;
 XX
 DT 08-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify ORF35 of Neisseria species.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW treatment; Neisseria infection; meningitis; septicaemia; gonorrhea;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Neisseria sp.
 XX
 XX WO9924578-A2.
 PN
 XX 20-MAY-1999.
 PD
 XX
 XX 09-OCT-1998; 98WO-IB01665.
 PF
 XX
 XX 01-SEP-1998; 98GB-0019016.
 PR 06-NOV-1997; 97GB-0023516.
 PR 14-NOV-1997; 97GB-0024190.
 PR 18-NOV-1997; 97GB-0024386.
 PR 27-NOV-1997; 97GB-0025158.
 PR 10-DEC-1997; 97GB-0026147.
 PR 14-JAN-1998; 98GB-0000759.
 XX
 XX (CHIR-) CHIRON SPA.
 PA
 XX
 XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
 PI WPI; 1999-327407/27.
 XX
 DR
 XX
 XX Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
 PT diagnosis, treatment and prevention of infection
 PT
 XX
 XX Disclosure; Page 489; 524pp; English.
 PS
 XX
 XX PCR primers AAX12359-Z12531 were used to amplify various open reading
 CC frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae. These
 CC ORFs (AAZ11972-Z12358) encode antigenic proteins (AAZ38499-Y38944). The

CC antigenic proteins, their fragments, their nucleic acids and antibodies
 CC are used for diagnosis, prevention (as vaccines) or treatment of
 CC *Neisseria* infections, such as meningitis, septicemia and gonorrhea.
 CC Both organisms are closely related. Fragments of the nucleic acids are
 CC useful as hybridisation probes and antisense reagents.

XX Sequence 30 BP; 5 A; 10 C; 8 G; 7 T; 0 other;
 SQ

Query Match 67.8%; Score 12.2; DB 20; Length 30;
 Best Local Similarity 82.4%; Pred. No. 3.9e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ctgagcactaaagctgg 18
 ||||| || |||||
 Db 27 CTGAGCTCTGAAGCTAG 11

RESULT 13
 AAZ55464/C
 ID AAZ55464 standard; DNA; 30 BP.

XX AAZ55464;

XX 21-MAR-2000 (first entry)

XX *Neisseria* species ORF cloning PCR primer #849.

XX *Neisseria* meningitidis; *Neisseria* gonorrhoeae; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
 KW antibacterial; gene therapy; PCR primer; ss.

OS Synthetic.

OS *Neisseria* sp.

XX WO9957280-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US09346.

XX 01-MAY-1998; 98US-0083758.

XX 31-JUL-1998; 98US-0094869.

XX 02-SEP-1998; 98US-0098994.

XX 02-SEP-1998; 98US-0099062.

XX 09-OCT-1998; 98US-0103749.

XX 09-OCT-1998; 98US-0103794.

XX 09-OCT-1998; 98US-0103796.

XX 25-FEB-1999; 99US-0121528.

XX (CHIR) CHIRON CORP.

XX (GENO-) INST GENOMIC RES.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;

XX Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

XX Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

XX Novel *Neisseria* polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics -

XX Example 16; Page 164; 1453pp; English.

XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAZ74253 to AAY75941
 CC represent novel *Neisseria* meningitis and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the

CC presence of *Neisseria* bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.

XX Sequence 30 BP; 5 A; 10 C; 8 G; 7 T; 0 other;

Query Match 67.8%; Score 12.2; DB 21; Length 30;
 Best Local Similarity 82.4%; Pred. No. 3.9e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ctgagcactaaagctgg 18
 ||||| || |||||
 Db 27 CTGAGCTCTGAAGCTAG 11

RESULT 14
 AAQ92440
 ID AAQ92440 standard; DNA; 38 BP.

XX AAQ92440;

XX 11-JAN-1996 (first entry)

XX TCR gamma constant region 5' PCR detection primer.

XX Primer; PCR; amplification; natural killer cell; purification; CD3; CD5;
 KW antibody; interleukin; proliferation; target cell type; beta-actin;
 KW allogenic lymphoblastoid; T-cell receptor; gene expression; ss.

OS Synthetic.

XX US5415874-A.

XX 16-MAY-1995.

XX 31-OCT-1989; 89US-0429353.

XX 31-OCT-1989; 89US-0429353.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Bender JR, Engleman EG, Pardi R;

XX WPI; 1995-193394/25.

XX Prodn. of target cell-specific natural killer cells - by selecting
 PT natural killer cells based on their adhesion to a selected target
 PT cell type and culturing.

XX Example 5; Column 15; 23pp; English.

XX Primers AAQ92434-49 were used to PCR detect specific messenger RNAs in
 CC cultured natural killer (NK) cells. The NK cells are purified by
 CC partial purification through a nylon wool column followed by removal
 CC of the CD3+ and CD5+ cells by incubating in the presence of bound
 CC anti-CD3 and anti-CD5 antibodies. The remaining cells which express
 CC the Leu1c+ (CD16) and Leu19 markers are enriched by propagating in a
 CC medium containing an agent e.g. interleukin (IL)-2 which promotes
 CC proliferation of the NK cells and in the presence of the NK cells,
 CC target cell type e.g. allogenic lymphoblastoid cells.

CC Confirmation of the correct NK cell type is carried by PCR amplification
 CC of the CD3 and T-cell receptor (TCR) markers alpha, beta, gamma and
 CC delta, on reverse transcribed RNA isolated from the NK cells. The
 CC primers AAQ92440-1 target the T-cell receptor gene gamma constant
 CC region.

XX Sequence 38 BP; 12 A; 9 C; 8 G; 9 T; 0 other;

Query Match 67.8%; Score 12.2; DB 16; Length 38;
 Best Local Similarity 82.4%; Pred. No. 4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctg 17
 ||||| 1 1
Db 7 tctgagcactagattg 23

RESULT 15
AAH43130/c
ID AAH43130 standard; CDNA; 39 BP.
XX
AC AAH43130;
XX
DT 17-OCT-2001 (first entry)
XX
DE Primer: F5-alpha-top.
XX
KW T cell receptor; TCR; influenza A; ligand; functional processing;
KW affinity; polymerase chain reaction; primer; amplify; PCR; ss.
XX
OS Synthetic.
XX
PN EP1118661-Al.
XX
PD 25-JUL-2001.
XX
PF 13-JAN-2000; 2000EP-0200110.
XX
PR 13-JAN-2000; 2000EP-0200110.
XX
PA (HETN-) HET NEDERLANDS KANKER INST.
XX
PI Schumacher ANM, Kessels HWHG;
XX
DR WPI; 2001-459002/50.
XX

Generating receptors with desired specificities for ligands, which upon binding to the ligand under-goes functional processing in order to provide a biological response after ligand-binding -
XX
PS Disclosure; Page 6; 21pp; English.
XX

CC The sequences given in AAH43128-34 are primers which were used in the amplification and cloning of the complementarity determining regions (CDR3) of a T cell receptor which was generated by the method of the invention. The method of the invention allows generation of receptors with desired specificities for ligands, which upon binding to the ligand under-go functional processing in order to provide a biological response after ligand-binding. The method is used for generating libraries of cells with receptors of differing affinities.
XX
SQ Sequence 39 BP; 10 A; 9 C; 9 G; 11 T; 0 other;

Query Match 66.7%; Score 12; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 cactaaagctgg 18
 |||||
Db 39 CACTAAAGCTGG 28

Search completed: October 12, 2002, 17:08:01
Job time: 9746 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:34 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

Sequence: 1 tctgagcactaaagctgg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	12.2	67.8	27	4	US-08-584-040-4947	Sequence 4947, Ap
2	11.8	65.6	28	4	US-09-129-686-14	Sequence 14, Appl
3	11.8	65.6	34	4	US-08-532-657A-11	Sequence 11, Appl
4	11.6	64.4	30	1	US-08-321-613-9	Sequence 9, Appl
5	11.6	64.4	38	3	US-08-850-961-3	Sequence 3, Appl
6	11.6	64.4	38	4	US-09-479-776-3	Sequence 3, Appl
7	11.4	63.3	22	1	US-08-609-572-9	Sequence 9, Appl
8	11.4	63.3	22	4	US-08-841-751-9	Sequence 9, Appl
9	11.4	63.3	22	4	US-08-846-344-9	Sequence 9, Appl
10	11.4	63.3	22	4	US-08-846-344-9	Sequence 9, Appl
11	11.4	63.3	25	3	US-08-343-998-12	Sequence 12, Appl
12	11.2	62.2	21	1	US-07-922-723A-30	Sequence 30, Appl
13	11.2	62.2	21	1	US-07-799-828C-30	Sequence 30, Appl
14	11.2	62.2	21	2	US-07-952-277A-30	Sequence 30, Appl
15	11.2	62.2	25	3	US-09-132-541-10	Sequence 10, Appl
16	11.2	62.2	27	1	US-08-758-306-164	Sequence 164, Appl
17	11.2	62.2	27	1	US-08-758-306-708	Sequence 708, Appl
18	11.2	62.2	27	1	US-08-758-306-720	Sequence 720, Appl
19	11.2	62.2	27	1	US-08-758-306-746	Sequence 746, Appl
20	11.2	62.2	27	1	US-08-758-306-1116	Sequence 1116, Ap
21	11.2	62.2	27	1	US-08-758-306-1136	Sequence 1136, Ap
22	11.2	62.2	27	2	US-08-956-242-12	Sequence 12, Appl
23	11.2	62.2	27	3	US-08-985-162-1115	Sequence 1115, Ap
24	11.2	62.2	27	3	US-08-985-162-1220	Sequence 1220, Ap
25	11.2	62.2	27	3	US-09-351-215-12	Sequence 12, Appl
26	11.2	62.2	27	3	US-08-998-099-144	Sequence 144, Appl
27	11.2	62.2	27	3	US-08-998-099-220	Sequence 220, Appl

Sequence 280, Appl
Sequence 82, Appl
Sequence 806, Appl
Sequence 3177, Ap
Sequence 3392, Ap
Sequence 3524, Ap
Sequence 3713, Ap
Sequence 3735, Ap
Sequence 4714, Ap
Sequence 4822, Ap
Sequence 5106, Ap
Sequence 5822, Ap
Sequence 6345, Ap
Sequence 6683, Ap
Sequence 6685, Ap
Sequence 6827, Ap
Sequence 7036, Ap
Sequence 7080, Ap

ALIGNMENTS

RESULT 1
US-08-584-040-4947
; Sequence 4947, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4947:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```
;
; FEATURE:
; OTHER INFORMATION: The letter "N" represents the stem II region
; OTHER INFORMATION: of an HH ribozyme.
; US-08-584-040-4947

Query Match          67.8%; Score 12.2; DB 4; Length 27;
Best Local Similarity 61.1%; Pred. No. 2.9e+02;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
   :|:| | | |||||:|
Db 8 UCUGAUGAAGAACGUGG 25

RESULT 2
US-09-129-686-14
; Sequence 14, Application US/09129686A
; Patent No. 6264940
; GENERAL INFORMATION:
; APPLICANT: Gromeier PhD, Matthias
; APPLICANT: Wimmer Prof, Eckard
; TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer
; FILE REFERENCE: Recomb Poliovirus for Cancer Treatment
; CURRENT APPLICATION NUMBER: US/09/129,686A
; CURRENT FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Poliovirus Type 1 Mahoney
; US-09-129-686-14

Query Match          65.6%; Score 11.8; DB 4; Length 28;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
   | ||||| |||||
Db 3 cggagcaataaagct 17

RESULT 3
US-08-532-657A-11/c
; Sequence 11, Application US/08532657A
; Patent No. 6346414
; GENERAL INFORMATION:
; APPLICANT: JACOBS, Eric
; TITLE OF INVENTION: TRANSDUCTION ASSEMBLY FOR GENE TRANSFER
; TITLE OF INVENTION: IN EUKARYOTES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,657A
; FILING DATE: 16-OCT-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: WO PCT/FR94/00419
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: FR 93/04530
; FILING DATE: 16-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 017753-069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: synthetic oligonucleotide
; US-08-532-657A-11

Query Match          65.6%; Score 11.8; DB 4; Length 34;
Best Local Similarity 86.7%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16
   | ||||| |||||
Db 21 CAGAGCACTGAAGCT 7

RESULT 4
US-08-321-613-9
; Sequence 9, Application US/08321613
; Patent No. 5789247
; GENERAL INFORMATION:
; APPLICANT: BALLAY, ANNICK
; APPLICANT: BOFFA, GEORGES
; APPLICANT: CARTRON, JEAN-PIERRE
; APPLICANT: CHRETEIN, STANY
; APPLICANT: LAMBIN, PATRICK
; APPLICANT: LOPEZ, CLAUDE
; APPLICANT: SALMON, CHARLES
; TITLE OF INVENTION: EXPRESSION IN NON-TUMORAL HUMAN
; TITLE OF INVENTION: LYMPHOBLASTOID LINES WITH AN INTEGRATIVE VECTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,613
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1217-130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
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;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-321-613-9

Query Match 64.4%; Score 11.6; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
||| ||||| ||| ||
Db 5 TCTAAGCACTTGAGCAGG 22

RESULT 5
US-08-850-961-3
; Sequence 3, Application US/08850961
; Patent No. 6013517
; GENERAL INFORMATION:
; APPLICANT: Respass, James G.
; APPLICANT: De Polo, Nicholas J.
; APPLICANT: Chada, Sunil
; APPLICANT: Sauter, Sybille
; APPLICANT: Bodner, Mordechai
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: CROSSLESS RETROVIRAL VECTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation, Intellectual Property - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850.961
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 6013517/man J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 930049.424C4 / 1147.005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-3520
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-850-961-3

Query Match 64.4%; Score 11.6; DB 3; Length 38;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
||| ||||| ||| ||
Db 10 TCTGAGAATTAAGGCTAG 27

RESULT 6
US-09-479-776-3
; Sequence 3, Application US/09479776

; Patent No. 6333195
; GENERAL INFORMATION:
; APPLICANT: Respass, James G.
; APPLICANT: De Polo, Nicholas J.
; APPLICANT: Chada, Sunil
; APPLICANT: Sauter, Sybille
; APPLICANT: Bodner, Mordechai
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: CROSSLESS RETROVIRAL VECTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY-R440
; P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,776
; FILING DATE: 07-Jan-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KRUSE, NORMAN J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 930049.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)622-4900
; TELEFAX: (206)682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-479-776-3

Query Match 64.4%; Score 11.6; DB 4; Length 38;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
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Db 10 TCTGAGAATTAAGGCTAG 27

RESULT 7
US-08-609-572-9
; Sequence 9, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-609-572-9

Query Match 63.3%; Score 11.4; DB 1; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaa 13
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DB 3 TCTGAGCAATAAA 15

RESULT 8
US-08-841-751-9
; Sequence 9, Application us/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-841-751-9

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaa 13
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DB 3 TCTGAGCAATAAA 15

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US-08-846-340-9
; Sequence 9, Application us/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; US-08-846-340-9

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy 1 tctgagcactaaa 13
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Db 3 TCTGAGCAATAAA 15

RESULT 10
US-08-846-344-9
; Sequence 9, Application US/08846344
; Patent No. 6268480
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
US-08-846-344-9

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctgagcactaaa 13
    ||||| ||||
Db 3 TCTGAGCAATAAA 15

RESULT 11
US-08-343-998-12
; Sequence 12, Application US/08343998A
; Patent No. 6020123
; GENERAL INFORMATION:
; APPLICANT: Sonigo, Pierre
; APPLICANT: Brechot, Christian
; APPLICANT: Courgnard, Valerie
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES FOR THE AMPLIFICATION OF THE
; TITLE OF INVENTION: GENOME OF THE RETROVIRUSES OF THE HIV-2 AND SIV TYPE,
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; TITLE OF INVENTION: AND THEIR USES FOR IN VITRO DIAGNOSIS OF THE INFECTIONS
; TITLE OF INVENTION: DUE TO THESE VIRUSES
; FILE REFERENCE: 2356.0065-01
; CURRENT APPLICATION NUMBER: US/08/343,998A
; CURRENT FILING DATE: 1994-11-18
; EARLIER APPLICATION NUMBER: 07/920,600
; EARLIER FILING DATE: 1992-01-22
; EARLIER APPLICATION NUMBER: PCT/FR90/00394
; EARLIER FILING DATE: 1990-06-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 2
; FEATURE:
US-08-343-998-12

Query Match 63.3%; Score 11.4; DB 3; Length 25;
Best Local Similarity 92.3%; Pred. No. 8.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ctgagcactaaaag 14
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Db 12 ctgtgactaaaag 24

RESULT 12
US-07-922-723A-30/c
; Sequence 30, Application US/07922723A
; Patent No. 5369004
; GENERAL INFORMATION:
; APPLICANT: Drs. Mihael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, Leblanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/922,723A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34506
; REFERENCE/DOCKET NUMBER: 717081B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-922-723A-30

Query Match 62.2%; Score 11.2; DB 1; Length 21;
Best Local Similarity 81.2%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 3 tgagcactaaagctgg 18
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Db 21 TGCACACTAAGGCTGG 6

RESULT 13
US-07-799-828C-30/c
; Sequence 30, Application US/07799828C
; Patent No. 5378602
; GENERAL INFORMATION:
; APPLICANT: Drs. Carl R. Merrill and
; APPLICANT: Michael H. Polymeropoulos
; TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE
; TITLE OF INVENTION: MICROSTATELLITE REPEAT
; TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; FILING DATE: 19911127
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 717081A
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-799-828C-30

Query Match 62.2%; Score 11.2; DB 1; Length 21;
Best Local Similarity 81.2%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgagcactaaagctgg 18
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Db 21 TGCACACTAAGGCTGG 6

RESULT 14
US-07-952-277A-30/c
; Sequence 30, Application US/07952277A
; Patent No. 5861504
; GENERAL INFORMATION:
; APPLICANT: Drs. Michael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
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; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: DOS Text File
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; APPLICATION NUMBER: US/07/952,277A
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34506
; REFERENCE/DOCKET NUMBER: 717081C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-952-277A-30

Query Match 62.2%; Score 11.2; DB 2; Length 21;
Best Local Similarity 81.2%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgagcactaaagctgg 18
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Db 21 TGCACACTAAGGCTGG 6

RESULT 15
US-09-132-541-10/c
; Sequence 10, Application US/09132541A
; Patent No. 6114113
; GENERAL INFORMATION:
; APPLICANT: MCLAUGHLIN-TAYLOR, Elizabeth
; APPLICANT: KRUGER, Mark
; APPLICANT: LUNDAK, Cheryl
; APPLICANT: KILLION, Catherine
; TITLE OF INVENTION: HIGH EFFICIENCY GENETIC MODIFICATION METHODS
; FILE REFERENCE: 1386.002
; CURRENT APPLICATION NUMBER: US/09/132,541A
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 60/055,453
; EARLIER FILING DATE: 1997-08-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This information is not availa
US-09-132-541-10

Query Match 62.2%; Score 11.2; DB 3; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Search completed: October 12, 2002, 16:54:35
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Job time: 8990 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-945-131-2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	13.8	76.7	25	62	US-60-233-166-390832
C 6	13.4	74.4	25	62	US-60-232-638-99211
C 7	13.4	74.4	25	62	US-60-232-638-99219
C 8	13.4	74.4	25	74	US-60-353-987-564374
C 9	13.4	74.4	25	74	US-60-353-987-889590
C 10	13.4	74.4	25	74	US-60-353-987-918095
11	13.4	74.4	50	1	PCT-US01-47856-2395
12	13.2	73.3	19	16	US-09-288-674-53
13	13.2	73.3	21	18	US-09-422-978-8397
C 14	13.2	73.3	21	74	US-60-350-061-525
C 15	13.2	73.3	24	29	US-09-754-853A-459
C 16	13.2	73.3	24	29	US-09-754-853A-461
C 17	13.2	73.3	25	35	US-09-954-427-410579
C 18	13.2	73.3	25	62	US-60-233-166-410579
C 19	13.2	73.3	25	62	US-60-234-049-46404
C 20	13.2	73.3	25	74	US-60-353-987-281238
C 21	13.2	73.3	25	74	US-60-353-987-594497
C 22	13.2	73.3	42	74	US-60-353-790-2578
C 23	13.2	73.3	47	47	US-60-082-614-236
C 24	13.2	73.3	47	47	US-60-082-614-889
C 25	13	72.2	25	62	US-60-234-049-88435
C 26	13	72.2	31	18	US-09-465-684-1427
C 27	13	72.2	41	17	US-09-313-221A-44
C 28	12.8	71.1	23	24	US-09-634-306B-176505
C 29	12.8	71.1	25	17	US-09-396-196F-53894
C 30	12.8	71.1	25	17	US-09-396-196F-69541
C 31	12.8	71.1	25	17	US-09-396-196F-84670

32 12.8 71.1 25 17 US-09-396-196F-105745, Sequence 105745,
c 33 12.8 71.1 25 35 US-09-956-584-491250, Sequence 491250,
c 34 12.8 71.1 25 35 US-09-956-584-491255, Sequence 491255,
35 12.8 71.1 25 62 US-60-232-638-17717, Sequence 17717, A
36 12.8 71.1 25 62 US-60-232-638-65760, Sequence 65760, A
37 12.8 71.1 25 62 US-60-232-638-98702, Sequence 98702, A
38 12.8 71.1 25 62 US-60-232-638-98714, Sequence 98714, A
39 12.8 71.1 25 62 US-60-232-638-107394, Sequence 107394,
40 12.8 71.1 25 62 US-60-232-638-107401, Sequence 107401,
c 41 12.8 71.1 25 62 US-60-234-017-517971, Sequence 517971,
c 42 12.8 71.1 25 62 US-60-234-017-517972, Sequence 517972,
43 12.8 71.1 25 74 US-60-353-987-729035, Sequence 729035,
44 12.8 71.1 47 60 US-60-216-745-3116, Sequence 3116, Ap
45 12.4 68.9 18 18 US-09-422-978-9233, Sequence 9233, Ap

ALIGNMENTS

RESULT 1
US-09-241-561-2
; Sequence 2, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-2

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
Db 1 tctgagcactaaagctgg 18

RESULT 2
US-60-232-638-45566
; Sequence 45566, Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLIC INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YDL187C
US-60-232-638-45566

Query Match 77.8%; Score 14; DB 62; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 tgagcactaaagct 16
Db 11 tgagcactaaagct 24

RESULT 3
US-09-396-196F-84671/c
; Sequence 84671, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84671
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-84671

Query Match 76.7%; Score 13.8; DB 17; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctgg 18
Db 20 CTGAGCACTAAATATGG 4

RESULT 4
US-09-954-427-390832/c
; Sequence 390832, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390832
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-09-954-427-390832

Query Match 76.7%; Score 13.8; DB 35; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctgg 18
||||| |||||||||

Db 22 CTGAGACCTAAAGCTGG 6

RESULT 5

US-60-233-166-390832/c
; Sequence 390832, Application US/60233166

; GENERAL INFORMATION:

; APPLICANT: Mittmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

; FILE REFERENCE: 3112

; CURRENT APPLICATION NUMBER: US/60/233,166

; CURRENT FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 420907

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 390832

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Affymetrix Proprieta

US-60-233-166-390832

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 62; Length 25;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctgg 18

||||| |||||||||

Db 22 CTGAGACCTAAAGCTGG 6

RESULT 6

US-60-232-638-99211/c

; Sequence 99211, Application US/60232638

; GENERAL INFORMATION:

; APPLICANT: Mittmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast

; FILE REFERENCE: 3110

; CURRENT APPLICATION NUMBER: US/60/232,638

; CURRENT FILING DATE: 2000-09-14

; NUMBER OF SEQ ID NOS: 138410

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 99211

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YLR196W

US-60-232-638-99211

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 62; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16

||||| |||||||||

Db 25 CAGAGCACTAAAGCT 11

RESULT 7

US-60-232-638-99219/c

; Sequence 99219, Application US/60232638

; GENERAL INFORMATION:

; APPLICANT: Mittmann

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast

; FILE REFERENCE: 3110

; CURRENT APPLICATION NUMBER: US/60/232,638

; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99219

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: SGD YLR196W

US-60-232-638-99219

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 62; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16

||||| |||||||||

Db 19 CAGAGCACTAAAGCT 5

RESULT 8

US-60-353-987-564374/c

; Sequence 564374, Application US/60353987

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

; FILE REFERENCE: 3121

; CURRENT APPLICATION NUMBER: US/60/353,987

; CURRENT FILING DATE: 2002-02-01

; NUMBER OF SEQ ID NOS: 997516

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 564374

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-60-353-987-564374

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 74; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctgagcactaaagct 16

||||| |||||||||

Db 16 CTGATCACTAAAGCT 2

RESULT 9

US-60-353-987-889590/c

; Sequence 889590, Application US/60353987

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

; FILE REFERENCE: 3121

; CURRENT APPLICATION NUMBER: US/60/353,987

; CURRENT FILING DATE: 2002-02-01

; NUMBER OF SEQ ID NOS: 997516

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 889590

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-60-353-987-889590

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 74; Length 25;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaagc 15

||||| |||||||||

Db 17 TCTGAGTACTAAAGC 3

```
RESULT 10
US-60-353-987-918095/c
; Sequence 918095, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 918095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-353-987-918095

Query Match          74.4%; Score 13.4; DB 74; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgcagcactaaagctg 17
   ||||| ||||| ||
Db 20 TGAGCACTAAAGGTG 6

RESULT 11
PCT-US01-47856-2395
; Sequence 2395, Application PC/TUS0147856
; GENERAL INFORMATION:
; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Quertermous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 506612000140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2395
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47856-2395

Query Match          74.4%; Score 13.4; DB 1; Length 50;
Best Local Similarity 93.3%; Pred. No. 8.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gagcactaaagctg 18
   ||| ||||| |||||
Db 17 gagcactaaagctg 31

RESULT 12
US-09-288-674-53
; Sequence 53, Application US/09288674
; GENERAL INFORMATION:
; APPLICANT: Freeman, Thomas C.
; APPLICANT: Richardson, Peter J.
; APPLICANT: Dickson, Alistair K.
; TITLE OF INVENTION: REVERSE TRANSCRIPTION AND AMPLIFICATION PROCESSES AND
; FILE REFERENCE: HLBB-6
; CURRENT APPLICATION NUMBER: US/09/288,674
; CURRENT FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: GB 98/17055.8
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; OTHER INFORMATION: primer
US-09-288-674-53

Query Match          73.3%; Score 13.2; DB 16; Length 19;
Best Local Similarity 83.3%; Pred. No. 9.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctg 18
   ||||| || ||||| ||
Db 1 tctgaccacaagaagctgg 18

RESULT 13
US-09-422-978-8397
; Sequence 8397, Application US/09422978
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020Cp1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8397
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-1515 for SEQ 532, in comple
US-09-422-978-8397

Query Match          73.3%; Score 13.2; DB 18; Length 21;
Best Local Similarity 83.3%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctg 18
   | ||||| ||||| ||
Db 2 tatgagcaccacaaggtgg 19

RESULT 14
US-60-350-061-525/c
; Sequence 525, Application US/60350061
; GENERAL INFORMATION:
```


; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; FILE REFERENCE: D0185
; CURRENT APPLICATION NUMBER: US/60/350,061
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-350-061-525

Query Match 73.3%; Score 13.2; DB 74; Length 21;
Best Local Similarity 83.3%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
| | | | | | | | | | | | | | | | | | | | | |
Db 18 TCTGAGCACTCAAGGAGG 1

RESULT 15
US-09-754-853A-459
; Sequence 459, Application US/09754853A
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 459
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 240017_region_G3_137548_13_Forward_Primer
US-09-754-853A-459

Query Match 73.3%; Score 13.2; DB 29; Length 24;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
| | | | | | | | | | | | | | | | | | | | | |
Db 2 tatgaaccctaaagctgg 19

Search completed: October 12, 2002, 20:42:29
Job time: 16399 sec

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:27 ; Search time 1154.93 Seconds
(without alignments) 52.829 Million cell updates/sec

Title: US-09-945-131-2

Perfect score: 18

Sequence: 1 tctgagcactaaagctgg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
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8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-2
2	13.8	76.7	25	5	US-09-396-196G-84671
3	13.4	74.4	50	6	US-10-131-831-2395
4	13.4	74.4	50	6	US-10-131-827-2395
5	13.2	73.3	19	6	US-10-019-906-16
6	13.2	73.3	19	6	US-10-019-906A-16
7	13.2	73.3	25	5	US-09-956-604-12259
8	13.2	72.2	25	5	US-09-956-604-107078
9	12.8	71.1	23	7	US-10-027-632-176505
10	12.8	71.1	25	5	US-09-396-196G-53894
11	12.8	71.1	25	5	US-09-396-196G-69541
12	12.8	71.1	25	5	US-09-396-196G-84670
13	12.8	71.1	25	5	US-09-396-196G-105745
14	12.4	68.9	20	1	PCT-US01-44838-533
15	12.4	68.9	25	5	US-09-396-196G-117149
16	12.4	68.9	32	1	PCT-US02-00335-5
17	12.4	68.9	50	6	US-10-131-831-2809
18	12.4	68.9	50	6	US-10-131-827-2809
19	12.2	67.8	25	5	US-09-956-604-141477
20	12.2	67.8	25	5	US-09-396-196G-17263
21	12.2	67.8	25	5	US-09-396-196G-39866
22	12.2	67.8	25	5	US-09-396-196G-83717
23	12.2	67.8	25	5	US-09-396-196G-95491
24	12.2	67.8	25	5	US-09-396-196G-118195
25	12.2	67.8	25	5	US-09-396-196G-122369

26	12.2	67.8	50	6	US-10-131-831-2599	Sequence 2599, Ap
27	12.2	67.8	50	6	US-10-131-827-2599	Sequence 2599, Ap
c 28	12	66.7	39	6	US-10-196-730-3	Sequence 3, Appli
c 29	11.8	65.6	21	1	PCT-US01-44838-648	Sequence 648, App
30	11.8	65.6	24	6	US-10-131-827-8918	Sequence 8918, Ap
c 31	11.8	65.6	25	5	US-09-956-604-16893	Sequence 16893, A
c 32	11.8	65.6	25	5	US-09-396-196G-53893	Sequence 53893, A
33	11.8	65.6	25	5	US-09-396-196G-69540	Sequence 69540, A
34	11.8	65.6	25	5	US-09-396-196G-105734	Sequence 105734
35	11.8	65.6	26	6	US-10-131-332A-8	Sequence 8, Appli
36	11.8	65.6	28	7	US-10-175-247-14	Sequence 14, Appli
37	11.8	65.6	36	5	US-09-601-997-16	Sequence 16, Appli
38	11.8	65.6	36	6	US-10-244-715-18	Sequence 18, Appli
39	11.8	65.6	37	7	US-10-138-674-20401	Sequence 20401, A
40	11.8	65.6	38	1	PCT-US02-23214-18	Sequence 18, Appli
41	11.8	65.6	38	6	US-10-197-816-18	Sequence 18, Appli
42	11.8	65.6	50	6	US-10-131-831-1761	Sequence 1761, Ap
43	11.8	65.6	50	6	US-10-131-831-1907	Sequence 1907, Ap
44	11.8	65.6	50	6	US-10-131-827-1761	Sequence 1761, Ap
45	11.8	65.6	50	6	US-10-131-827-1907	Sequence 1907, Ap

ALIGNMENTS

RESULT 1

US-09-945-131-2

; Sequence 2, Application US/09945131

; GENERAL INFORMATION:

; APPLICANT: SIROIS, Martin G.

; APPLICANT: EDELMAN, Elazar R.

; APPLICANT: ROSENBERG, Robert D.

; APPLICANT: SIMONS, Michael

; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing

; FILE REFERENCE: 12554.4

; CURRENT APPLICATION NUMBER: US/09/945,131

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Rattus rattus

; FEATURE:

; NAME/KEY: mRNA

; LOCATION: (1)..(18)

; OTHER INFORMATION: Antisense oligonucleotide

US-09-945-131-2

Query Match 100.0% Score 18; DB 5; Length 18;

Best Local Similarity 100.0%; Pred.No. 2.7; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0;

Qy 1 tctgagcactaaagctgg 18

Db 1 tctgagcactaaagctgg 18

RESULT 2

US-09-396-196G-84671/c

; Sequence 84671, Application US/09396196G

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84671
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-84671

Query Match 76.7%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ctgagcactaaagctgg 18
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Db 20 CTGAGCACTAAATATGG 4

RESULT 3
US-10-131-831-2395
; Sequence 2395, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2395
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2395

Query Match 74.4%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 gagcactaaagctgg 18
||| ||||| |||
Db 17 gagaactaaagctgg 31

RESULT 4
US-10-131-827-2395
; Sequence 2395, Application US/10131827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2395
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2395

Query Match 74.4%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 gagcactaaagctgg 18
||| ||||| |||
Db 17 gagaactaaagctgg 31

RESULT 5
US-10-019-906-16
; Sequence 16, Application US/10019906
; GENERAL INFORMATION:
; APPLICANT: Richardson, Peter
; APPLICANT: Cox, Peter
; TITLE OF INVENTION: A Method for Amplifying Low Abundance Nucleic Acid Sequences a
; FILE REFERENCE: GJE-83
; CURRENT APPLICATION NUMBER: US/10/019,906
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/144,666
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-019-906-16

Query Match 73.3%; Score 13.2; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tctgagcactaaagctgg 18
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Db 1 tctgaccacaagctgg 18

RESULT 6
US-10-019-906A-16
; Sequence 16, Application US/10019906A
; GENERAL INFORMATION:
; APPLICANT: Richardson, Peter
; APPLICANT: Cox, Peter
; TITLE OF INVENTION: A Method for Amplifying Low Abundance Nucleic Acid Sequences a
; FILE REFERENCE: GJE-83
; CURRENT APPLICATION NUMBER: US/10/019,906A
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/144,666
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: oligonucleotide
US-10-019-906A-16

Query Match 73.3%; Score 13.2; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
||||| || ||||| |||

Db 1 tctgaccacaagaagctgg 18

RESULT 7

US-09-956-604-12259

; Sequence 12259, Application US/09956604

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli

; FILE REFERENCE: 3117.1

; CURRENT APPLICATION NUMBER: US/09/956,604

; CURRENT FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/234,049

; PRIOR FILING DATE: 2000-09-19

; NUMBER OF SEQ ID NOS: 141629

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 12259

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Escherichia coli

US-09-956-604-12259

Query Match 73.3%; Score 13.2; DB 5; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctgagcactaaagctgg 18
||||| ||||| ||||| |||

Db 4 tcttaagactaaagctgg 21

RESULT 8

US-09-956-604-107078

; Sequence 107078, Application US/09956604

; GENERAL INFORMATION:

; APPLICANT: Mittmann, Michael

; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli

; FILE REFERENCE: 3117.1

; CURRENT APPLICATION NUMBER: US/09/956,604

; CURRENT FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/234,049

; PRIOR FILING DATE: 2000-09-19

; NUMBER OF SEQ ID NOS: 141629

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 107078

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Escherichia coli

US-09-956-604-107078

Query Match 72.2%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 gcactaaagctgg 18
||||| ||||| ||||| |||

Db 5 gcactaaagctgg 17

RESULT 9

US-10-027-632-176505/c

; Sequence 176505, Application US/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 176505

; LENGTH: 23

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-176505

Query Match 71.1%; Score 12.8; DB 7; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctgagcactaaagct 16
||||| ||||| ||||| |||

Db 17 TCTGAGCACACAGCT 2

RESULT 10

US-09-396-196G-53894/c

; Sequence 53894, Application US/09396196G

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 53894

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-53894

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctgagcactaaagct 16
||||| ||||| ||||| |||

Db 20 TCTGAGCTCTACAGCT 5

RESULT 11

US-09-396-196G-69541
; Sequence 69541, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-69541

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctgagcactaaagctg 17
||| || |||||

Db 5 ctgtgcgctaaagctg 20

RESULT 12

US-09-396-196G-84670/c
; Sequence 84670, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84670
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-84670

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgagcactaaagctg 18
|||||

Db 25 TGAGCACAATAATGG 10

RESULT 13

US-09-396-196G-105745
; Sequence 105745, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-105745

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctgagcactaaagct 16
|||||

Db 5 tctgagcactataact 20

RESULT 14

PCT-US01-44838-533/c
; Sequence 533, Application PC/TUS0144838
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; TITLE OF INVENTION: Genetic Typing of Human Genes And Related Materials And Method
; FILE REFERENCE: 4389-23-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/44838
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 1449
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 533
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-44838-533

Query Match 68.9%; Score 12.4; DB 1; Length 20;
Best Local Similarity 92.9%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctgagcactaaag 14
|||||

Db 15 TCTGAGCACTAATG 2

RESULT 15

US-09-396-196G-117149/c
; Sequence 117149, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117149
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-117149

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctgagcactaaag 14
|||||||
Db 24 TCTGAGCACGAAAG 11

Search completed: October 12, 2002, 17:27:28
Job time: 10803 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:13 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-3

Perfect score: 18

Sequence: 1 gtgatagatgccgagca 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c	2	12.2	67.8	20	6	AX080276	AX080276 Sequence
c	3	12.2	67.8	21	6	AX111202	AX111202 Sequence
c	4	12.2	67.8	37	6	AR008967	AR008967 Sequence
c	5	12	66.7	27	6	ARI43811	ARI43811 Sequence
c	6	11.6	64.4	30	6	AX100540	AX100540 Sequence
c	7	11.4	63.3	30	6	AX17582	AX17582 oligonucleo
c	8	11.4	63.3	36	9	HSTCARB2	HSTCARB2 H.sapiens (
c	9	11.4	63.3	45	6	E60002	E60002 Ceramide-bi
c	10	11.4	63.3	45	10	MUSTCRBCAB	M80440 Mouse T-cel
c	11	11.2	62.2	19	6	AX354589	AX354589 Sequence
c	12	11.2	62.2	20	6	AX057501	AX057501 Sequence
c	13	11.2	62.2	20	6	AX119428	AX119428 Sequence
c	14	11.2	62.2	20	6	AX119528	AX119528 Sequence
c	15	11.2	62.2	21	6	AR091447	AR091447 Sequence
c	16	11.2	62.2	24	6	I26952	I26952 Sequence 1
c	17	11.2	62.2	24	6	I28388	I28388 Sequence 1
c	18	11.2	62.2	24	6	I96080	I96080 Sequence 1
c	19	11.2	62.2	25	6	I33604	I33604 Sequence 26
c	20	11.2	62.2	27	6	AR047936	AR047936 Sequence
c	21	11.2	62.2	28	6	AX057466	AX057466 Sequence
c	22	11.2	62.2	30	6	AX2595	AX2595 Sequence 11
c	23	11.2	62.2	30	6	AB8783	AB8783 Sequence 93
c	24	11.2	62.2	30	6	AR001285	AR001285 Sequence
c	25	11.2	62.2	30	6	AR003602	AR003602 Sequence
c	26	11.2	62.2	30	6	AR025286	AR025286 Sequence
c	27	11.2	62.2	30	6	AR037092	AR037092 Sequence
c	28	11.2	62.2	30	6	AR063120	AR063120 Sequence
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c	30	11.2	62.2	30	6	AR164690	AR164690 Sequence
c	31	11.2	62.2	30	6	I24824	I24824 Sequence 6
c	32	11.2	62.2	30	6	I35448	I35448 Sequence 15
c	33	11.2	62.2	31	6	AX248210	AX248210 Sequence
c	34	11.2	62.2	34	6	AR044274	AR044274 Sequence
c	35	11.2	62.2	34	6	I35914	I35914 Sequence 15
c	36	11.2	62.2	34	6	I68887	I68887 Sequence 15
c	37	11.2	62.2	45	6	AR026954	AR026954 Sequence
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c	39	11.2	62.2	48	6	AR044207	AR044207 Sequence
c	40	11.2	62.2	48	6	AR044208	AR044208 Sequence
c	41	11.2	62.2	48	6	I35847	I35847 Sequence 47
c	42	11.2	62.2	48	6	I35848	I35848 Sequence 48
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ALIGNMENTS

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LOCUS						
DEFINITION			T-cell receptor variable delta 1 [human, T lymphocytes, mRNA			
ACCESSION			S54891			
VERSION			S54891.1	GI:264828		
KEYWORDS			human T lymphocytes.			
SOURCE			Homo sapiens			
ORGANISM			Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE			1 (bases 1 to 45)			
AUTHORS			Shimonkevitz,R., Colburn,C., Burnham,J.A., Murray,R.S. and Kotzin,B.L.			
TITLE			Clonal expansions of activated gamma/delta T cells in recent-onset multiple sclerosis			
JOURNAL			Proc. Natl. Acad. Sci. U.S.A. 90 (3), 923-927 (1993)			
MEDLINE			93157384			
REMARK			GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 124257] from the original journal article.			
FEATURES			This sequence comes from Fig. 2.			
			Location/Qualifiers			

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RESULT 6
AX100540/c
LOCUS AX100540 30 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 5 from Patent WO0121785.
ACCESSION AX100540
VERSION AX100540.1 GI:13619544
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE
1 (bases 1 to 30)
AUTHORS Jefferson,R.A., Yang,W. and Grossnicklaus,U.
TITLE Megagametophyte transcriptional control elements and uses thereof
JOURNAL Patent: WO 0121785-A 5 29-MAR-2001;
Cambia (AU); COLD SPRING HARBOR LABORATORY (US); JEFFERSON,
Richard Anthony (AU); Yang, Wei (AU); Grossnicklaus, Ueli (CH)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
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Query Match 64.4%; Score 11.6; DB 6; Length 30;
Best Local Similarity 77.8%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtgtagtagtgcgcgacga 18
||||| ||| |||
Db 27 GTGATATTAGCTAAGCA 10

RESULT 7
AL17582
LOCUS AL17582 30 bp DNA linear PAT 23-MAR-1994
DEFINITION Oligonucleotide primer OBVD 8 location on BVDV genome 1808 - 1837.
ACCESSION AL17582
VERSION AL17582.1 GI:513082
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE
1 (bases 1 to 30)
AUTHORS Belak,S. and Ballagi-Pordany,A.
TITLE A method of detecting an infection caused by a specific type of
virus, primers, probes and a test kit
JOURNAL Patent: EP 0464010-A 6 02-JAN-1992;
STATENS VETERINARMEDICINSKA ANSTALT
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 3 a 10 c 5 g 12 t
ORIGIN
Query Match 63.3%; Score 11.4; DB 6; Length 30;
Best Local Similarity 92.3%; Pred. No. 7.5e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 tagtatgcgcgacg 17
||||| |||
Db 10 TAGTATCCCGAGC 22

RESULT 8
HSTCARB2
LOCUS HSTCARB2 36 bp mRNA linear PRI 28-JUN-1995

```

```

DEFINITION H.sapiens (BDE20) mRNA for T-cell antigen receptor-beta.
ACCESSION Z35671
VERSION Z35671.1 GI:527467
KEYWORDS T-cell antigen receptor-beta.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 36)
AUTHORS Lehner,P.J.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1994) Paul J. Lehner Dr., Medicine, Tenovus
Building, University of, Wales College of Medicine, Heath Park,
Cardiff, South Glamorgan, CF4 4XN, Wales, UK
REFERENCE
2 (bases 1 to 36)
AUTHORS Lehner,P.J., Wang,E.C., Moss,P.A., Williams,S., Platt,K.,
Friedman,S.M., Bell,J.I. and Borysiewicz,L.K.
TITLE Human HLA-A*0201-restricted cytotoxic T lymphocyte recognition of
Influenza A is dominated by T cells bearing the V beta 17 gene
segment
JOURNAL J. Exp. Med. 181 (1), 79-91 (1995)
MEDLINE 95105732
FEATURES
source
1..36
Location/Qualifiers
/organism="Homo sapiens"
/isolate="BD"
/db_xref="taxon:9606"
/clone="BDE20"
/cell_type="cytotoxic T lymphocyte"
<1..>36
/codon_start=1
/product="T-cell antigen receptor VJ junction beta chain"
/protein_id="CAA84740.1"
/db_xref="GI:527468"
/translation="CASSMRSSSQHF"
misc_feature 9..30
BASE COUNT 7 a 9 c 11 g 9 t
ORIGIN
Query Match 63.3%; Score 11.4; DB 9; Length 36;
Best Local Similarity 92.3%; Pred. No. 7.5e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 tagtatgcgcgacg 17
||||| |||
Db 9 TAGTATCGGAGC 21

RESULT 9
E60002/c
LOCUS E60002 45 bp DNA linear PAT 31-JAN-2002
DEFINITION Ceramide-binding peptide.
ACCESSION E60002
VERSION E60002.1 GI:18622761
KEYWORDS JP 2000319296-A/2
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE
1 (bases 1 to 45)
AUTHORS Ishikawa,M., Tanaka,Y., Ogino,K. and Taki,T.
TITLE Ceramide-binding peptide
JOURNAL Patent: JP 2000319296-A 2 21-NOV-2000;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Artificial Sequence
PN JP 2000319296-A/2
PD 21-NOV-2000
PF 10-MAY-1999 JP 1999128674
PI MASARU ISHIKAWA, YOSHINORI TANAKA, KOICHI OGINO, TAKAO TAKI
CC C07K7/00

```

```

FH Key Location/Qualifiers
FT source 1..45 /organism='Artificial Sequence'
FEATURES
Source 1..45 Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2 a 8 c 19 g 16 t
ORIGIN
Query Match 63.3%; Score 11.4; DB 6; Length 45;
Best Local Similarity 92.3%; Pred. No. 7.5e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 agtagccgagca 18
|||||
Db 21 AGTAGCCGAACA 9
RESULT 10
MUSTCRBCAB 45 bp mRNA linear ROD 29-MAR-1999
LOCUS Mouse T-cell receptor beta-chain mRNA V-D-J junction region,
partial cds.
ACCESSION M80440 S74646
VERSION M80440.1 GI:201843
KEYWORDS D-region; J-region; T-cell receptor beta-chain CDR3; V-region;
processed gene.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Adams,S., Leblanc,P. and Datta,S.K.
TITLE Functional region sequences of T-cell receptor beta-chain genes
expressed by pathogenic anti-DNA autoantibody-inducing helper T
cells from lupus mice: possible selection by cationic autoantigens
Proc. Natl. Acad. Sci. U.S.A. 88 (24), 11271-11275 (1991)
JOURNAL 92107931
MEDLINE
COMMENT On Mar 29, 1999 this sequence version replaced gi:241313.
FEATURES
Source 1..45 Location/Qualifiers
/organism="Mus musculus"
/strain="(SWR x NZB)F1"
/db_xref="taxon:10090"
/cell_line="L-9.2"
/cell_type="T helper cell hybridoma"
/tissue_type="lymphoid"
<1..>45
CDS /codon_start=1
/product="T-cell receptor beta"
/protein_id="AAA51246.1"
/db_xref="GI:201844"
/translation="CASSDQYAEQFFGP"
<1..14
V_region /note="V-beta-8.3"
D_segment 15..21 /note="D-beta-N"
J_segment 22..>45 /note="J-beta-2.1"
BASE COUNT 9 a 10 c 14 g 12 t
ORIGIN
Query Match 63.3%; Score 11.4; DB 10; Length 45;
Best Local Similarity 92.3%; Pred. No. 7.5e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 agtagccgagca 18
|||||
Db 20 AGTAGCTGAGCA 32

```

```

RESULT 11
LOCUS AX354589/c 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 36 from Patent WO0179555.
ACCESSION AX354589
VERSION AX354589.1 GI:18619391
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE
AUTHORS Hancock,W.W. and Ozkaynak,E.
TITLE Roles of Jak/stat family members in tolerance induction
JOURNAL Patent: WO 0179555-A 36 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Source 1..19 Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 3 a 6 c 3 g .7 t
ORIGIN
Query Match 62.2%; Score 11.2; DB 6; Length 19;
Best Local Similarity 81.2%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 gatagtgcgagca 18
|||||
Db 19 GACAGTATGATGAGCA 4
RESULT 12
LOCUS AX057501/c 20 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 37 from Patent WO0077204.
ACCESSION AX057501
VERSION AX057501.1 GI:12310235
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Lorenz,E., Schwartz,D.A. and Schutte,B.C.
TITLE Variant tlr4 nucleic acid and uses thereof
JOURNAL Patent: WO 0077204-A 37 21-DEC-2000;
University of Iowa Research Foundation (US) ; Lorenz, Eva (US)
FEATURES
Source 1..20 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 4 a 7 c 3 g 6 t
ORIGIN
Query Match 62.2%; Score 11.2; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 gatagtgcgagca 18
|||||
Db 18 GTTAGAATGCTGAGCA 3
RESULT 13
LOCUS AX119428 20 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 85 from Patent WO0129251.
ACCESSION AX119428
VERSION AX119428.1 GI:14036347

```

KEYWORDS SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nfl gene
JOURNAL Patent: WO 0129251-A 85 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 5 a 2 c 7 g 6 t
ORIGIN
Query Match 62.2%; Score 11.2; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 gtgatatgtatgccgag 16
||| ||||| |||
Db 3 GTTATTGTATGCGGAG 18
RESULT 14
AX119528
LOCUS AX119528 20 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 185 from Patent WO0129251.
ACCESSION AX119528
VERSION AX119528.1 GI:14036447
KEYWORDS human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nfl gene
JOURNAL Patent: WO 0129251-A 185 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 5 a 2 c 7 g 6 t
ORIGIN
Query Match 62.2%; Score 11.2; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 gtgatatgtatgccgag 16
||| ||||| |||
Db 3 GTTATTGTATGCGGAG 18
RESULT 15
AR091447
LOCUS AR091447 21 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 11 from patent US 5994119.
ACCESSION AR091447
VERSION AR091447.1 GI:10018202
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
Dietz,H.C.
TITLE Mammalian regulator of nonsense-mediated RNA decay

JOURNAL Patent: US 5994119-A 11 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..21
BASE COUNT 5 a 5 c 7 g 4 t
ORIGIN
Query Match 62.2%; Score 11.2; DB 6; Length 21;
Best Local Similarity 81.2%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 tgatatgtatgccgagc 17
||| ||||| |||
Db 4 TCACAGGATGCGAGGC 19
Search completed: October 12, 2002, 16:51:15
Job time: 8890 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:01 ; Search time 792.17 Seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-3

Perfect score: 18
Sequence: 1 gtgatagatgccgagca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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- 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
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- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AA13834	Murine PDGFR-beta
2	12.8	71.1	47	AAQ94496	Human antibody ONS
3	12.8	71.1	47	AAT38611	Chimaeric human/mu
4	12.2	67.8	20	AAF63623	Isogenic transgeni
5	12.2	67.8	21	AAH01942	parC resistance ge
6	12.2	67.8	37	AAQ81544	Antisense primer f
7	12	66.7	21	AAV51618	Zea mays genome fo
8	12	66.7	27	AA227099	Saccharomyces cere
9	11.8	65.6	21	AAH40980	CAP marker primer

10	11.8	65.6	46	21	AA151720	PCR primer 194-89
11	11.6	64.4	25	24	ABK16565	Short tandem repea
12	11.6	64.4	30	22	AAF77637	A thaliana enhance
13	11.6	64.4	34	22	AA161133	Human VEGF-B10-108
14	11.6	64.4	42	22	AAH41016	PCR primer specifi
15	11.6	64.4	47	21	AAZ67522	Human map-related
16	11.4	63.3	26	17	AAQ03660	Osteoblast prolife
17	11.4	63.3	30	13	AAQ20364	Primer OBVD8 from
18	11.4	63.3	45	22	AAF25920	Ceramide affinity
19	11.2	62.2	19	24	AAZ43330	Human Stat1 amplif
20	11.2	62.2	20	22	AAQ04985	Neurofibromatosis
21	11.2	62.2	20	22	AAQ05085	Neurofibromatosis
22	11.2	62.2	20	22	AAQ84801	Human TLR4 gene ex
23	11.2	62.2	21	18	AAZ96720	Human RENT1 primer
24	11.2	62.2	24	13	AAQ29498	EDA-FN primer (1)
25	11.2	62.2	25	18	AAZ59971	Primer PC24 for P
26	11.2	62.2	27	16	AAQ04253	Primer #1 for TA a
27	11.2	62.2	28	22	AAZ84770	Human TLR4 exon 2/
28	11.2	62.2	29	15	AAQ55954	COL2A1 3'-primer (
29	11.2	62.2	30	16	AAQ83378	c-fos antisense ol
30	11.2	62.2	33	24	ABA05584	Human Pax protein
31	11.2	62.2	39	21	AAA26591	Human HPC1 mutatio
32	11.2	62.2	41	22	AAI65255	Human dihydrorota
33	11.2	62.2	45	16	AAQ75899	CDR-grafting prime
34	11.2	62.2	50	22	AAZ82527	Human SNP oligonuc
35	11	61.1	12	23	AB144725	Oligonucleotide pr
36	11	61.1	19	15	AAQ57322	Enzymatic RNA mole
37	11	61.1	25	21	AAZ82987	HHV6 detecting PCR
38	11	61.1	25	22	AAH03056	Microorganism dete
39	11	61.1	28	20	AAZ35844	Antisense oligonuc
40	10.8	60.0	17	22	AAH95229	Human Chk1 ribozym
41	10.8	60.0	17	22	AAH95518	Human Chk1 ribozym
42	10.8	60.0	17	22	AAH95729	Human Chk1 ribozym
43	10.8	60.0	17	22	AAH95978	Human Chk1 ribozym
44	10.8	60.0	19	22	AAZ45444	Primer #148 used i
45	10.8	60.0	20	20	AAZ93233	PCR primer used to

ALIGNMENTS

RESULT 1
AA13834
ID AAA13834 standard; DNA; 18 BP.

XX AAA13834;

AC AAA13834;

DT 27-JUL-2000 (first entry)

XX Murine PDGFR-beta scrambled control oligonucleotide SEQ ID NO:3.

XX Murine; mouse; platelet derived growth factor receptor beta; vasotropic;

XX PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;

XX recurrent stenosis; cardiovascular injury; ss.

XX Mus sp.

XX key Location/Qualifiers

FT modified_base 1..18

FT /*tag= a

FT /note= "phosphorothioate linkages"

XX CA2228977-A1.

XX 07-MAY-1999.

XX 03-FEB-1998; 98CA-2228977.

XX 07-NOV-1997; 97CA-2215360.

XX (EDEL/) EDELMAN E R.

XX (ROSE/) ROSENBERG R D.

XX (SIRO/) SIROIS M G.

PA (SIMO/) SIMONS M.
 XX Edelman ER, Rosenberg RD, Sirois MG, Simons M;
 XX WPI; 2000-283933/25.
 XX Antisense inhibition of platelet derived growth factor beta-receptor
 PT subunit expression for the prevention of restenosis -
 XX Example 1; Page 15; 43pp; English.
 XX A method has been developed for preventing restenosis following vascular
 CC injury by antisense inhibition of platelet derived growth factor
 CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
 CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
 CC canal), especially of a valve in the heart, after surgical correction of
 CC the primary condition) following cardiovascular injury. The present
 CC sequence represents a scrambled control phosphorothioate oligonucleotide
 CC for murine PDGFR-beta, which is used in an example from the present
 CC invention.
 XX Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.57; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgatatgacgcagca 18
 ||||| ||||| ||||| |||||
 Db 1 gtgatatgacgcagca 18

RESULT 2
 AAQ94496
 ID AAQ94496 standard; DNA; 47 BP.
 XX AAQ94496;
 XX 16-JAN-1996 (first entry)
 XX Human antibody ONS-M21 CDR PCR primer F.
 XX Human; ONS-M21 antibody; chimeric protein; CDR; medulloblastoma;
 KW brain tumour; treatment; diagnosis; PCR primer F;
 KW complementarity determining region; ss.
 XX Synthetic.
 OS WO9514041-A1.
 PN 26-MAY-1995.
 XX 19-OCT-1994; 94WO-JP01763.
 XX 19-NOV-1993; 93JP-0291078.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Ohtomo T, Sato K, Tsuchiya M;
 XX WPI; 1995-200347/26.
 XX Reconstituted antibody against human medullo:blastoma cells -
 PT contains high proportion of human antibody origin and has low
 PT antigenicity
 XX Example 5; Page 63; 120pp; Japanese.
 XX AAQ94492-094497 are human antibody ONS-M21 CDR PCR primers. The
 CC cDNA encoding the CDRs was used in the construction of an
 CC expression vector, contg. cDNA encoding a human/murine chimeric
 CC antibody, reactive with human medulloblastoma (a brain tumour)

CC cells. The chimeric antibody can be used in the diagnosis and
 CC treatment of this disease.
 XX Sequence 47 BP; 12 A; 12 C; 14 G; 9 T; 0 other;
 SQ

Query Match 71.1%; Score 12.8; DB 16; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18
 ||||| ||||| ||||| |||||
 Db 17 gatagtatgccgagta 32

RESULT 3
 AAT38611
 ID AAT38611 standard; DNA; 47 BP.
 XX AAT38611;
 XX 09-DEC-1996 (first entry)
 XX Chimaeric human/murine MAB ONS-M21 PCR primer G.
 XX Murine; human; myeloblastoma; chimaera; monoclonal antibody;
 KW chimera; single stranded Fv region; PCR; low human antigenicity;
 KW diagnosis; treatment; cerebral tumour; reshaped; primer;
 KW polymerase chain reaction; ss.
 XX Synthetic.
 OS JP08169900-A.
 PN 02-JUL-1996.
 XX 18-NOV-1994; 94JP-0285057.
 XX 18-OCT-1994; 94JP-0252166.
 XX 19-NOV-1993; 93JP-0291078.
 XX (CHUS) CHUGAI PHARM CO LTD.
 XX WPI; 1996-358509/36.
 XX Reshaped anti-human myeloblastoma cell human antibody - has low
 PT human antigenicity, and is therefore useful for diagnosis and
 PT treatment of cerebral tumours, e.g. myeloblastoma
 XX Example 5; Page 23; 45pp; Japanese.
 XX The present sequence is a primer for the chimaeric human/murine
 CC monoclonal antibody (MAB) ONS-M21. The MAB was prepd. by combining
 CC light and heavy variable region DNA, from a murine anti-human
 CC myeloblastoma cell MAB, with human light and heavy constant region
 CC sequences, respectively to produce chimaeric human/murine light and
 CC heavy chain DNA mols.. A recombinant vector for the expression of
 CC the heavy and light chain DNA mols. was prepd., and used to
 CC transform a host cell. The host cell was then cultured, and the
 CC expression prods. of the heavy and light chain DNA mols. sepd. and
 CC connected with a peptide linker to produce a single stranded Fv
 CC region. The reshaped Fv region has low human antigenicity, and is
 CC therefore expected to be useful as an agent for the diagnosis and
 CC treatment of cerebral tumours, e.g. myeloblastoma.
 XX Sequence 47 BP; 12 A; 12 C; 14 G; 9 T; 0 other;
 SQ

Query Match 71.1%; Score 12.8; DB 17; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18

Db 17 gatagatgccgagta 32
||||| ||||||| I

RESULT 4

AAF63623/c
ID AAF63623 standard; DNA; 20 BP.

XX
AC AAF63623;

XX 04-MAY-2001 (first entry)

XX Isogenic transgenic plant line related oligo LB2 SEQ ID NO:3.

XX Isogenic transgenic plant; line; T-DNA; transformation; cross-breeding;
KW hybrid; plant; characterisation; amplification; PCR primer; ss.

XX Plantae.

OS Synthetic.

XX WO200107632-A1.

XX 01-FEB-2001.

XX 25-JUL-2000; 2000WO-FR02130.

XX 28-JUL-1999; 99FR-0009990.

XX (RHOB-) RHOBIO.

XX Perez P, Garcia D;

XX WPI; 2001-168557/17.

XX Production of transgenic plant lines, useful for producing elite
PT hybrids with transgenic characteristics, includes selection for
PT incorporation of transgene into particular parent

XX Example 3; Page 18; 44pp; French.

XX The present invention describes a method for the production of isogenic
CC transgenic plant lines (A) by transforming cells of a hybrid with T-DNA
CC vector containing a transgene (I), the hybrid being derived by crossing
CC a line of interest (II) and a line suitable for transformation (LT).
CC Primary transformants are selected for integration of T-DNA into the LI
CC genome only, then back-crossed with LI and selection of products until
CC (A) are obtained. The method is used for introgression of several
CC transgenic characteristics into a plant. (I) may express an antisense
CC RNA, ribozyme or protein that confers resistance to disease or pathogens
CC and/or improves some agronomic or nutritional property. By selecting
CC primary transformants, the method allows introduction of genes without
CC additional fragments (representing a genetic burden) bound to the
CC transgene, i.e. it makes possible production of truly isogenic
CC lines while retaining an acceptable efficiency of transfer. The speed
CC with which (I) can be transferred to a plant genome is increased, since
CC the number of backcrossings required is reduced and the genetic sources
CC for production of commercial hybrids is significantly broadened. The
CC present sequence represents a PCR primer for amplifying a left border
CC (LB) sequence in an example from the present invention.

XX Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 other;

Query Match 67.8%; Score 12.2; DB 22; Length 20;

Best Local Similarity 82.4%; Pred. No. 1.5e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy. 1 gtgagatgatgccgagc 17

||||| I |||||||

Db 17 GTGATTTCGCGGACC 1

RESULT 5

AAH01942/c
ID AAH01942 standard; DNA; 21 BP.

XX
AC AAH01942;

XX 24-JUL-2001 (first entry)

XX parC resistance gene detection nucleotide sequence SEQ ID NO:1935.

XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasiticol;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial;
KW vaccine; primer; ss.

XX Unidentified.

XX WO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-CA01150.

XX 28-SEP-1999; 99CA-2283458.

XX 19-MAY-2000; 2000CA-2307010.

XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

XX Picard FJ, Roy PH;

XX WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasiticol species in a test sample -
XX Claim 21; Page 1414; 1580pp; English.

XX The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasiticol
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasiticol species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexA nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.

XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

Query Match 67.8%; Score 12.2; DB 22; Length 21;

Best Local Similarity 82.4%; Pred. No. 1.5e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtgatagtatgccgagc 17
 || |||||
 Db 18 GTCGAAGTATGCCGAGC 2

RESULT 6
 AAQ81544
 ID AAQ81544 standard; cDNA; 37 BP.

XX AC AAQ81544;

XX DT 07-OCT-1995 (first entry)

XX DE Antisense primer for adeno virus 5 fiber sequence.

XX KW DNA primer; adeno virus; ss; CD30 ligand; Hodgkins lymphoma;
 XX KW gene therapy.

XX OS Synthetic.

XX PN W09505201-A.

XX PD 23-FEB-1995.

XX PF 11-AUG-1994; 94WO-US09172.

XX PR 13-AUG-1993; 9305-0106078.

XX PA (GENE-) GENETIC THERAPY INC.

XX PI McClelland A, Stevenson SC;

XX DR WPI; 1995-098586/13.

XX PT Adenovirus comprising fibre protein contg. a ligand - specific
 XX PT for cell surface receptor, used to treat Hodgkin's lymphoma.

XX PS Example 4; Page 29; 71pp; English.

XX CC The DNA primer, specific for the adeno virus 5 fiber gene, is used
 CC with sense primer AAQ81543 in the construction of plasmid p680.2
 CC containing adeno virus 5 fiber genes. This plasmid can be used to
 CC direct substitutions of modified adeno virus 5 fiber genes into YAC,
 CC and ultimately in the construction of plasmid pGEM5r:CD30L and a
 CC recombinant adeno virus expressing a 5F:CD30 ligand chimera. The
 CC recombinant adeno virus vector is used for in vivo transduction of
 CC cells expressing the LDL receptor e.g. liver cells, for CD30 ligand
 CC gene expression in vivo. Preferably, adeno virus 5 has residues
 CC 400-581 replaced with CD30 ligand cDNA. This process is used for the
 CC treatment of Hodgkins lymphoma, adenosine-deaminase deficiency,
 CC sickle cell anaemia, thalassaemia, alpha-antitrypsin deficiency,
 CC Alzheimer disease, phenylketonuria, growth disorders and heart
 CC disease by gene therapy.

XX SQ Sequence 37 BP; 11 A; 10 C; 9 G; 7 T; 0 other;

Query Match 67.8%; Score 12.2; DB 16; Length 37;
 Best Local Similarity 82.4%; Pred. No. 1.6e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatagtatgccgagca 18
 ||||| |||||
 Db 21 tgatcatcatgacgagca 37

RESULT 7
 AAV51618
 ID AAV51618 standard; DNA; 21 BP.

XX AC AAV51618;

XX XX 02-FEB-1999 (first entry)

XX DE

XX Zea mays genome forward PCR primer #218.

XX KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; corn; ss.

XX OS Synthetic.

XX OS Zea mays.

XX PN W09824796-A1.

XX PD 11-JUN-1998.

XX PF 01-DEC-1997; 97WO-US21782.

XX PR 07-MAR-1997; 97US-0813507.

XX PR 02-DEC-1996; 96US-0032069.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Landry BS, Lemieux B, Murigneux A, Sapolsky RJ;

XX DR WPI; 1998-333252/29.

XX KW Brassica species allele-specific oligonucleotide probes and primers
 PT - useful for plant breeding

XX PS Example 1; Page Page 53; 65pp; English.

XX CC AAV51401-V51704 are forward PCR primers used to amplify fragments of the
 CC Zea mays genome in order to detect polymorphic markers. Such markers can
 CC be used in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution
 CC of an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a
 CC back-crossed plant with an ancestral plant.

XX SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 other;

Query Match 66.7%; Score 12; DB 19; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 agtatgccgagc 17

Db ||||| |||||

6 agtatgccgagc 17

RESULT 8

AAZ27099/c

ID AAZ27099 standard; DNA; 27 BP.

XX AC AAZ27099;

XX DT 19-NOV-1999 (first entry)

XX DE Saccharomyces cerevisiae DNA-binding protein target sequence #70.

XX KW DNA binding protein; DBP; zinc finger; 2F domain; target; ss.

XX OS Saccharomyces cerevisiae.

XX PN W09942474-A2.

XX PD 26-AUG-1999.

XX PF 19-FEB-1999; 99WO-US03692.

XX PR 20-FEB-1998; 98US-0075466.

XX XX

SQ Sequence 46 BP; 18 A; 5 C; 14 G; 9 T; 0 other;

Query Match 65.6%; Score 11.8; DB 21; Length 46;
Best Local Similarity 86.7%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtgatagatgccga 15
||||| ||||| |||
Db 19 gtgacgtatgacga 33

RESULT 11

ABK16565/c
ID ABK16565 standard; DNA; 25 BP.

XX
AC ABK16565;

XX
DT 14-MAR-2002 (first entry)

XX Short tandem repeat loci detection, multiplex PCR primer #42.

XX Multiplex PCR; short tandem repeat; STR; amelogenin;

KW Combined DNA index system; CODIS; PCR primer;

KW locus specific bracket; LSB; locus specific allelic ladder; ss.

XX Synthetic.

XX
PN W0200192575-A1.

XX
PD 06-DEC-2001.

XX
XX 23-MAY-2001; 2001WO-US16547.

XX
PR 30-MAY-2000; 2000US-0580497.

XX
PA (OLIG-) OLIGOTRAIL LLC.

XX
PI Dau PC, Liu D;

XX
DR WPI; 2002-090048/12.

XX Determining the alleles at several loci in a DNA-containing sample,
PT useful for analysing short tandem repeat genetic markers in a genomic
PT system, by multiplex PCR of thirteen Combined DNA Index System (CODIS)
PT loci and amelogenin

XX
PS Claim 18; Page 33; 164pp; English.

XX The invention describes a novel method of determining the alleles
CC present at several loci in a DNA-containing sample. The method comprises
CC amplifying by multiplex PCR the thirteen specific and distinct
CC polymorphic short tandem repeat (STR) genetic loci of the Combined DNA
CC Index System (CODIS) and amelogenin for sex determination. The method is
CC useful for detecting and analysing short tandem repeat (STR) genetic
CC markers in a genomic system. The length of amplified alleles can be
CC determined using both internal and external lane calibration standards,
CC including locus specific brackets (LSB) and locus specific allelic
CC ladders respectively. This sequence is one of 43 PCR primers
CC (ABK16524-ABK16566) designed to amplify the STR's in a genomic sample,
CC described in the method of the invention.

XX
SQ Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 other;

Query Match 64.4%; Score 11.6; DB 24; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtgatagatgccga 18
||||| ||| | ||||
Db 18 GTGATACCATGTCAGCA 1

RESULT 12

AAF77637/c
ID AAF77637 standard; DNA; 30 BP.

XX
AC AAF77637;

XX
DT 29-MAY-2001 (first entry)

XX A thaliana enhancer element PCR primer SEQ ID NO: 5.

XX Megagametophyte transcriptional control element; enhancer element;
KW female gametophyte specific gene expression; cereal; PCR primer; ss.

XX Arabidopsis thaliana.

XX
PN W0200121785-A2.

XX
PD 29-MAR-2001.

XX
PF 20-SEP-2000; 2000WO-US26359.

XX
PR 20-SEP-1999; 99US-0155361.

XX (CMB-) CAMBIA.

XX (COLD-) COLD SPRING HARBOR LAB.

XX (JEFF/) JEFFERSON R A.

XX (YANG/) YANG W.

XX (GROS/) GROSSNICKLAUS U.

XX Jefferson RA, Yang W, Grossnicklaus U;

XX WPI; 2001-257983/26.

XX New plant transformation vector for expression of structural genes,
PT comprises an enhancer element operably linked to a nucleotide sequence
PT of interest, operative in a plant megagametophyte

XX Example 3; Page 41; 48pp; English.

XX The present invention describes a plant transformation vector comprising
CC an enhancer element operative in a plant megagametophyte, where the
CC enhancer is operably linked to a coding sequence of interest. This is
CC useful for promoting the expression of sequences of interest in the
CC female gametophyte only, particularly in cereals such as rice.

XX
SQ Sequence 30 BP; 10 A; 9 C; 4 G; 7 T; 0 other;

Query Match 64.4%; Score 11.6; DB 22; Length 30;
Best Local Similarity 77.8%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtgatagatgccga 18

Db 27 GTGATATTAGGCTAAGCA 10

RESULT 13

AAD16133/c
ID AAD16133 standard; DNA; 34 BP.

XX
AC AAD16133;

XX
DT 19-NOV-2001 (first entry)

XX Human VEGF-B10-108 mature DNA amplifying 5' primer.

XX Protein purification; affinity chromatography; angiogenesis;

KW vascular endothelial growth factor; autotransplantation; tumour;

KW rheumatoid arthritis; diabetic retinopathy; human;

KW VEGF-B10-108; PCR primer; ss.

XX

```

OS Homo sapiens.
PN WO200160861-A1.
XX
XX 23-AUG-2001.
PD
XX
XX 16-FEB-2001; 2001WO-AU00160.
XX PF
XX 16-FEB-2000; 2000AU-0005681.
XX PR
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
PA
XX
XX Scrofani SDB, Nash AD, Fabri LJ, Mackenzie AW, Scotney PD;
PI
XX WPI; 2001-541645/60.
DR
XX Purifying a protein or polypeptide, e.g. vascular endothelial growth
PT factor (VEGF)-B isoform, comprises subjecting a biological sample to
PT affinity chromatography to allow the full length to bind and not the
PT truncated or clipped forms -
XX
XX Example 21; Page 36; 77pp; English.
PS
XX The invention relates to a method for purifying a polypeptide comprising
CC subjecting a biological sample to chromatography with an affinity matrix
CC for an N- or C-terminal region of the polypeptide, that permits binding
CC of full length molecule and not the truncated form. The method is useful
CC for purifying human vascular endothelial growth factor (VEGF) especially
CC VEGF-B isoforms e.g. VEGF-B167, VEGF-B186 and VEGF-B108. VEGF is
CC involved in normal angiogenesis including formation of the corpus luteum,
CC placental development, regulation of vascular permeability, inflammatory
CC angiogenesis, autotransplantation and human diseases such as tumour
CC promoting angiogenesis, rheumatoid arthritis and diabetes related
CC retinopathy. The VEGF molecules are useful in therapeutic protocols and
CC diagnostic assays. The present sequence is a PCR primer used for
CC amplifying mature human VEGF-B10-108 DNA.
XX
XX Sequence 34 BP; 12 A; 11 C; 8 G; 3 T; 0 other;
SQ
Query Match 64.4%; Score 11.6; DB 22; Length 34;
Best Local Similarity 77.8%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 gtgatagatgctgcgagca 18
DB 24 GTGATAGTGTGCTGCGGA 7
RESULT 14
AAH41016/C
ID AAH41016 standard; DNA; 42 BP.
XX
XX AAH41016;
AC
XX
XX 23-AUG-2001 (first entry)
DT
XX
XX PCR primer specific for human metalloprotease DNA.
DE
XX
XX Metalloprotease; human; aggrecanase; joint disease; osteoarthritis;
KW osteopathic; antiarthritic; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200134785-A1.
PN
XX
XX 17-MAY-2001.
PD
XX
XX 10-NOV-2000; 2000WO-JP07917.
XX PF
XX
XX 11-NOV-1999; 99JP-0321740.
XX PR
XX 16-MAY-2000; 2000JP-0144020.
XX

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PA (YAMA ) YAMANOUCHI PHARM CO LTD.
PA (KAZU-) KAZUSA DNA RES INST.
XX
PI Yamaji N, Nishimura K, Abe K, Ohara O, Nagase T, Nomura N;
XX
XX WPI; 2001-343602/36.
DR
XX
XX Metalloprotease with aggrecanase activity for treating joint diseases
PT especially osteoarthritis -
PT
XX
XX Example 4; Page 62; 85pp; Japanese.
PS
XX This invention relates to a metalloprotease with aggrecanase activity.
CC The invention includes protein and DNA sequences of the metalloprotease,
CC vectors containing the DNA, host cells transformed by the vectors, and
CC antibodies directed against the metalloprotease. The antibodies, protein
CC and DNA sequences can be used in the treatment and prevention of joint
CC diseases, particularly osteoarthritis. The treatment may result in
CC osteopathic and antiarthritic activity. The present sequence represents
CC a PCR primer used in the isolation and characterisation of the
CC metalloprotease gene of the invention.
XX
XX Sequence 42 BP; 6 A; 12 C; 11 G; 13 T; 0 other;
SQ
Query Match 64.4%; Score 11.6; DB 22; Length 42;
Best Local Similarity 77.8%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 gtgatagatgctgcgagca 18
DB 37 GGGTTAGGATGCCAGCA 20
RESULT 15
AAZ67522
ID AAZ67522 standard; DNA; 47 BP.
XX
XX AAZ67522;
AC
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human map-related biallelic marker SEQ ID NO:1869.
DE
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
OS
XX
XX Key variation Location/Qualifiers
FT replace(24,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO9954500-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-IB00822.
XX PF
XX
XX 21-APR-1998; 98US-0082614.
XX PR
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX
XX WPI; 2000-013267/01.
DR
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
PT

```

XX Claim 1; Page 629; 2745pp; English.
PS
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 17 A; 7 C; 12 G; 11 T; 0 other;

.Query Match 64.4%; Score 11.6; DB 21; Length 47;
Best Local Similarity 77.8%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gtgatagatgccgagca 18
Db 22 gggaaagtatgctcgagaa 39

Search completed: October 12, 2002, 17:08:02
Job time: 9747 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:35 ; Search time 191.26 seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-3
Perfect score: 18
Sequence: 1 gtgatagtagcgagca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.8	71.1	47	4	US-08-646-265A-40
2	12.2	67.8	37	1	US-08-591-492-16
3	12	66.7	27	4	US-09-253-396A-73
4	11.8	65.6	46	3	US-09-235-246-16
5	11.4	63.3	26	3	US-08-604-965E-14
6	11.4	63.3	26	3	US-08-604-965E-20
7	11.2	62.2	21	2	US-08-724-354D-11
8	11.2	62.2	21	3	US-09-270-984A-11
9	11.2	62.2	24	1	US-08-244-494A-1
10	11.2	62.2	24	1	US-08-119-231-1
11	11.2	62.2	24	1	US-08-628-343-1
12	11.2	62.2	25	1	US-08-448-204-26
13	11.2	62.2	27	1	US-08-207-481-13
14	11.2	62.2	27	5	PCT-US95-02689-13
15	11.2	62.2	30	1	US-07-789-179-6
16	11.2	62.2	30	1	US-08-240-712-15
17	11.2	62.2	30	1	US-08-443-890-15
18	11.2	62.2	30	1	US-08-444-942-6
19	11.2	62.2	30	1	US-08-446-105-6
20	11.2	62.2	30	1	US-08-444-939-6
21	11.2	62.2	30	2	US-08-444-991-6
22	11.2	62.2	30	2	US-08-450-733-6
23	11.2	62.2	30	4	US-09-058-562-15
24	11.2	62.2	30	4	US-08-444-915A-6
25	11.2	62.2	30	5	PCT-US92-09752-15
26	11.2	62.2	34	1	US-08-411-795B-155
27	11.2	62.2	34	1	US-08-411-796-155

c	28	11.2	62.2	34	1	US-08-469-319A-155	Sequence 155, App
c	29	11.2	62.2	34	3	PCT-US93-11198-155	Sequence 155, App
c	30	11.2	62.2	34	5	US-08-553-501A-39	Sequence 39, Appl
	31	11.2	62.2	45	2	US-09-205-231-39	Sequence 39, Appl
	32	11.2	62.2	45	3	US-08-411-795B-47	Sequence 47, Appl
	33	11.2	62.2	48	1	US-08-469-319A-47	Sequence 48, Appl
c	34	11.2	62.2	48	1	US-08-469-319A-48	Sequence 48, Appl
	35	11.2	62.2	48	1	US-09-311-260-80	Sequence 80, Appl
c	36	11.2	62.2	25	4	US-09-162-484-12	Sequence 12, Appl
	37	11	61.1	28	4	US-08-914-421-5	Sequence 5, Appl
	38	11	61.1	26	4	US-08-683-409-5	Sequence 5, Appl
	39	10.8	60.0	26	4	US-08-250-740-2	Sequence 2, Appl
	40	10.8	60.0	31	1	US-07-695-472B-12	Sequence 12, Appl
	41	10.8	60.0	31	1	US-08-066-961-42	Sequence 42, Appl
c	42	10.8	60.0	33	1	US-08-415-593-15	Sequence 15, Appl
c	43	10.8	60.0	41	2	US-08-485-355B-14	Sequence 14, Appl
	44	10.8	60.0	46	4		
	45	10.8	60.0				

RESULT 1

US-08-646-265A-40

; Sequence 40, Application US/08646265A

; Patent No. 6214973

; GENERAL INFORMATION:

; APPLICANT: OHTOMO, Toshihiko

; APPLICANT: SATO, Koh

; APPLICANT: TSUCHIYA, Masayuki

; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS

; NUMBER OF SEQUENCES: 132

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,265A

; FILING DATE: 09-SEP-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-291078

; FILING DATE: 19-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-291078

; FILING DATE: 19-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: WEGNER, Harold C.

; REGISTRATION NUMBER: 25,258

; REFERENCE/DOCKET NUMBER: 53466/184

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 47 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-646-265A-40

ALIGNMENTS

Query Match 71.1%; Score 12.8; DB 4; Length 47;
Best Local Similarity 87.5%; Pred. No. 97;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gatagtagccgagca 18
||||| |||||||
Db 17 GATAGGATCCGAGTA 32

RESULT 2

US-08-591-492-16
; Sequence 16, Application US/08591492
; Patent No. 5736086
; GENERAL INFORMATION:
; APPLICANT: McClelland, Alan
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Adenoviruses Having Modified
; TITLE OF INVENTION: Fiber Proteins
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,492
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,078
; FILING DATE: 13-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: PCR DNA primer
US-08-591-492-16

Query Match 67.8%; Score 12.2; DB 1; Length 37;
Best Local Similarity 82.4%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tgatagtagccgagca 18
||||| ||| |||||
Db 21 TGATATCATGACGAGCA 37

RESULT 3

US-09-253-396A-73/c
; Sequence 73, Application US/09253396A
; Patent No. 6205404
; GENERAL INFORMATION:
; APPLICANT: Genome Dynamics, Inc.
; TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Class
; FILE REFERENCE: 1116242-0003 file: genome03f.app

; CURRENT APPLICATION NUMBER: US/09/253,396A
; CURRENT FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-253-396A-73

Query Match 66.7%; Score 12; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 gtatgcccagca 18
||||| |||||||
Db 14 GTATGCCGAGCA 3

RESULT 4

US-09-235-246-16
; Sequence 16, Application US/09235246A
; Patent No. 6048719
; GENERAL INFORMATION:
; APPLICANT: Kong, Hulmin
; APPLICANT: Higgins, Lauren S.
; APPLICANT: Dalton, Michael A.
; TITLE OF INVENTION: Method For Cloning And Producing The DraIII Restriction
; TITLE OF INVENTION: Endonuclease
; FILE REFERENCE: DraIII
; CURRENT APPLICATION NUMBER: US/09/235,246A
; CURRENT FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Deinococcus radiophilus
US-09-235-246-16

Query Match 65.6%; Score 11.8; DB 3; Length 46;
Best Local Similarity 86.7%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtgatgtagtgcgca 15
||||| ||||| |||
Db 19 gtgatgtagtgcgca 33

RESULT 5

US-08-604-965E-14/c
; Sequence 14, Application US/08604965E
; Patent No. 6046033
; GENERAL INFORMATION:
; APPLICANT: Goto, Masaaki
; APPLICANT: Tsuda, Eisuke
; APPLICANT: Yano, Kazuki
; APPLICANT: Kobayashi, Fumie
; APPLICANT: Yamaguchi, Kyoji
; APPLICANT: Washida, Naohiro
; APPLICANT: Satake, Toshiko
; APPLICANT: Morinaga, Tomonori
; APPLICANT: Ueda, Masatsugu
; APPLICANT: Higashio, Kanji
; TITLE OF INVENTION: Basic Osteoblast Growth FactorII(bOGF-
; TITLE OF INVENTION: II)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burgess, Ryan and Wayne
; STREET: 370 Lexington Avenue, Suite 2105
; CITY: NEW YORK

STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,965E
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEFAX: 212-532-4285
TELEX: 423794
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-604-965E-14

Query Match 63.3%; Score 11.4; DB 3; Length 26;
Best Local Similarity 92.3%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 agtatgccgagca 18
||||| |||||
Db 26 AGTATGCAGAGCA 14

RESULT 6
US-08-604-965E-20/c
Sequence 20, Application US/08604965E
Patent No. 6046033
GENERAL INFORMATION:
APPLICANT: Goto, Masaaki
APPLICANT: Tsuda, Eisuke
APPLICANT: Yano, Kazuki
APPLICANT: Kobayashi, Fumie
APPLICANT: Yamaguchi, Kyoji
APPLICANT: Washida, Naohiro
APPLICANT: Satake, Toshiko
APPLICANT: Morinaga, Tomonori
APPLICANT: Ueda, Masatsugu
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Basic Osteoblast Growth FactorII(DOGF-
TITLE OF INVENTION: II)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burgess, Ryan and Wayne
STREET: 370 Lexington Avenue, Suite 2105
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604,965E
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEFAX: 212-532-4285
TELEX: 423794
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-604-965E-20

Query Match 63.3%; Score 11.4; DB 3; Length 26;
Best Local Similarity 92.3%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 agtatgccgagca 18
||||| |||||
Db 26 AGTATGCAGAGCA 14

RESULT 7
US-08-724-354D-11
Sequence 11, Application US/08724354D
Patent No. 5994119
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-724-354D-11

Query Match 62.2%; Score 11.2; DB 2; Length 21;
Best Local Similarity 81.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatagtgcgcgacg 17
||| || ||| ||| |||
Db 4 TGACAGGATGCAGACG 19

RESULT 8

US-09-270-984A-11
; Sequence 11, Application US/09270984A
; Patent No. 6048965
; GENERAL INFORMATION:
; APPLICANT: Dietz, Harry C.
; TITLE OF INVENTION: MAMMALIAN REGULATOR OF
; TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,984A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/724,354
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-270-984A-11

Query Match 62.2%; Score 11.2; DB 3; Length 21;
Best Local Similarity 81.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatagtgcgcgacg 17
||| || ||| ||| |||
Db 4 TGACAGGATGCAGACG 19

RESULT 9

US-08-244-494A-1/c
; Sequence 1, Application US/08244494A
; Patent No. 5561114
; GENERAL INFORMATION:
; APPLICANT: KOMAI, Takahashi
; APPLICANT: MIYASHITA, Keiichi
; APPLICANT: SAKASHITA, Elji
; APPLICANT: KAMOGAWA, Hiroshi

; APPLICANT: INOUE, Fujio
; APPLICANT: TAKENISHI, Soichiro
; TITLE OF INVENTION: AN ADSORBENT FOR CELLULAR
; TITLE OF INVENTION: FIBRONECTIN, A METHOD FOR FRACTIONAL
; TITLE OF INVENTION: PURIFICATION OF FIBRONECTIN AND A
; TITLE OF INVENTION: METHOD OF HEMOCATHARSIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,494A
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 255199/1992
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGART, WADDELL A.
; REGISTRATION NUMBER: 24,861
; REFERENCE/DOCKET NUMBER: 035327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-244-494A-1

Query Match 62.2%; Score 11.2; DB 1; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtgtagtgatgcgcgag 16
||| || ||| ||| |||
Db 17 GTGATGGAATTCGAG 2

RESULT 10

US-08-119-231-1/c
; Sequence 1, Application US/08119231
; Patent No. 5571679
; GENERAL INFORMATION:
; APPLICANT: SEKIGUCHI, KIYOTOSHI
; APPLICANT: ASAKAWA, KANEJI
; APPLICANT: SAKASHITA, ELJI
; APPLICANT: HINO, KAZUO
; APPLICANT: SHIN, SADAHIRO
; APPLICANT: TACHIKAWA, TETSUYA
; APPLICANT: HIRANO, HISANOBU
; TITLE OF INVENTION: ANTI-EDA MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 PENNSYLVANIA AVE., NW
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/119,231
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 61524/1991
; FILING DATE: 26-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 157966/1991
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 286668/1991
; FILING DATE: 31-OCT-1991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-7060
; TELEFAX: 202-293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-119-231-1

Query Match 62.2%; Score 11.2; DB 1; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtgatgtatgccgag 16
DB 17 GTGATGAATCCGAG 2

RESULT 11
US-08-628-343-1/c
; Sequence 1, Application US/08628343
; Patent No. 5734025
; GENERAL INFORMATION:
; APPLICANT: KOMAI, Takahashi
; APPLICANT: MIYASHITA, Keiichi
; APPLICANT: SAKASHITA, Eiji
; APPLICANT: KAMOGAWA, Hiroshi
; APPLICANT: INOUE, Fujio
; APPLICANT: TAKENISHI, Soichiro
; TITLE OF INVENTION: AN ADSORBENT FOR CELLULAR
; TITLE OF INVENTION: FIBRONECTIN, A METHOD FOR FRACTIONAL
; TITLE OF INVENTION: PURIFICATION OF FIBRONECTIN AND A
; TITLE OF INVENTION: METHOD OF HEMOCATHARSIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,343
; FILING DATE: 05-APR-1996
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 255199/1992
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: PCT/JP93/01366
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: 08/244,494
; FILING DATE: 25-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGART, WADDELL, A.
; REGISTRATION NUMBER: 24,861
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-628-343-1

Query Match 62.2%; Score 11.2; DB 1; Length 24;
Best Local Similarity 81.2%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gtgatgtatgccgag 16
DB 17 GTGATGAATCCGAG 2

RESULT 12
US-08-448-204-26
; Sequence 26, Application US/08448204
; Patent No. 5593836
; GENERAL INFORMATION:
; APPLICANT: Niemiec, John
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detecting
; TITLE OF INVENTION: Pneumocystis carinii
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,204
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,089
; FILING DATE: 14-MAY-1993
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-08-448-204-26

Query Match 62.2%; Score 11.2; DB 1; Length 25;
Best Local Similarity 81.2%; Pred. No. 7.7e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 tgatgtatgccgagc 17
||||| ||||| |||
Db 2 TCATAAGATGCCGAGC 17

RESULT 13

US-08-207-481-13
Sequence 13, Application US/08207481

Patent No. 5820866

GENERAL INFORMATION:

APPLICANT: Kappler, John W.

APPLICANT: Marrack, Philippa

TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL

TITLE OF INVENTION: REGULATION

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: SHERIDAN ROSS & MCINTOSH

STREET: 1700 LINCOLN STREET, SUITE 3500

CITY: DENVER

STATE: COLORADO

COUNTRY: USA

ZIP: 80202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/207,481

FILING DATE: 04-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.

REGISTRATION NUMBER: 33,005

REFERENCE/DOCKET NUMBER: 2879-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/863-9700

TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-207-481-13

Query Match 62.2%; Score 11.2; DB 1; Length 27;

Best Local Similarity 81.2%; Pred. No. 7.8e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18
||| ||| ||||| |||
Db 6 GAGAGGATGCCGTGCA 21

RESULT 14

PCT-US95-02689-13

Sequence 13, Application PC/TUS9502689

GENERAL INFORMATION:

APPLICANT: National Jewish Center for Immunology and

APPLICANT: Respiratory Medicine

APPLICANT: Kappler, John W.

APPLICANT: Marrack, Philippa

TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL REGULATION

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: SHERIDAN ROSS & MCINTOSH

STREET: 1700 LINCOLN STREET, SUITE 3500

CITY: DENVER

STATE: COLORADO
COUNTRY: USA
ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02689
FILING DATE: 03-MAR-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.

REGISTRATION NUMBER: 33,005

REFERENCE/DOCKET NUMBER: 2879-8-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/863-9700

TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

PCT-US95-02689-13

Query Match 62.2%; Score 11.2; DB 5; Length 27;

Best Local Similarity 81.2%; Pred. No. 7.8e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 gatagtatgccgagca 18

||| ||| ||||| |||

Db 6 GAGAGGATGCCGTGCA 21

RESULT 15

US-07-789-179-6

Sequence 6, Application US/07789179

Patent No. 5545727

GENERAL INFORMATION:

APPLICANT: HOFFMAN, STEPHEN J.

APPLICANT: LOOKER, DOUGLAS L.

APPLICANT: ROSENDAHL, MARY S.

APPLICANT: STETLER, GARY L.

APPLICANT: WAGENBACH, MICHAEL

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHEWS, ANTONY J.

TITLE OF INVENTION: PRODUCTION AND USE OF HEMOGLOBIN AND

TITLE OF INVENTION: ANALOGUES THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 SEVENTH STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/789,179

FILING DATE: 19911108

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/07/671,707

FILING DATE: 01-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/374,161
FILING DATE: 30-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/379,116
FILING DATE: 13-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/349,623
FILING DATE: 10-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HOFFMAN-5B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-789-179-6

Query Match 62.2%; Score 11.2; DB 1; Length 30;
Best Local Similarity 81.2%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tgatagtatgccgagc 17
|||||
Db 12 TGATTGCATGCCGAAC 27

Search completed: October 12, 2002, 16:54:36
Job time: 8991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:29 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: us-09-945-131-3

Perfect score: 18
Sequence: 1 gtgatagtagtcgcgagca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	16	US-09-241-561-3	Sequence 3, Appli
2	14.4	80.0	25	62	US-60-234-049-123602	Sequence 123602,
3	13.4	74.4	25	35	US-09-954-427-357122	Sequence 357122,
4	13.4	74.4	25	35	US-09-954-427-357123	Sequence 357123,
5	13.4	74.4	25	35	US-09-954-427-357134	Sequence 357134,
6	13.4	74.4	25	35	US-09-954-429A-14687	Sequence 14687, A
7	13.4	74.4	25	35	US-09-954-429A-14688	Sequence 14688, A
8	13.4	74.4	25	35	US-09-954-429A-14689	Sequence 14689, A
9	13.4	74.4	25	35	US-09-956-584-141745	Sequence 141745,
10	13.4	74.4	25	62	US-60-233-166-357122	Sequence 357122,
11	13.4	74.4	25	62	US-60-233-166-357123	Sequence 357123,
12	13.4	74.4	25	62	US-60-233-166-357134	Sequence 357134,
13	13.4	74.4	25	62	US-60-233-357-17436	Sequence 17436, A
14	13.4	74.4	25	62	US-60-233-357-17437	Sequence 17437, A
15	13.4	74.4	25	62	US-60-233-357-17438	Sequence 17438, A
16	13.4	74.4	25	62	US-60-233-620-84925	Sequence 84925, A
17	13.4	74.4	25	62	US-60-233-620-84926	Sequence 84926, A
18	13.4	74.4	25	62	US-60-234-017-132654	Sequence 132654,
19	13.4	74.4	25	74	US-60-353-987-305023	Sequence 305023,
20	13.2	73.3	47	60	US-60-216-745-1570	Sequence 1570, Ap
21	13.2	73.3	50	29	US-09-755-374A-11926	Sequence 11926, A
22	13	72.2	25	74	US-60-353-987-533045	Sequence 533045,
23	12.8	71.1	25	35	US-09-954-427-180775	Sequence 180775,
24	12.8	71.1	25	35	US-09-954-427-306269	Sequence 306269,
25	12.8	71.1	25	35	US-09-956-584-278693	Sequence 278693,
26	12.8	71.1	25	62	US-60-233-166-180775	Sequence 180775,
27	12.8	71.1	25	62	US-60-233-166-306269	Sequence 306269,
28	12.8	71.1	25	62	US-60-234-017-266246	Sequence 266246,
29	12.8	71.1	25	74	US-60-353-987-916688	Sequence 916688,
30	12.8	71.1	47	26	US-09-671-317-523	Sequence 523, App
31	12.8	71.1	47	29	US-09-749-873-40	Sequence 40, Appl

32 12.4 68.9 25 35 US-09-954-427-357124
33 12.4 68.9 25 35 US-09-954-427-357125
34 12.4 68.9 25 35 US-09-954-429A-14686
35 12.4 68.9 25 35 US-09-954-429A-14690
36 12.4 68.9 25 35 US-09-956-584-22741
37 12.4 68.9 25 35 US-09-956-584-574177
38 12.4 68.9 25 35 US-09-956-584-574187
39 12.4 68.9 25 62 US-60-233-166-357124
40 12.4 68.9 25 62 US-60-233-166-357125
41 12.4 68.9 25 62 US-60-233-357-17435
42 12.4 68.9 25 62 US-60-233-357-17439
43 12.4 68.9 25 62 US-60-233-620-106965
44 12.4 68.9 25 62 US-60-234-017-42411
45 12.4 68.9 25 62 US-60-234-017-575065

ALIGNMENTS

RESULT 1

US-09-241-561-3
; Sequence 3. Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-3

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgatagatgcgcagca 18
| | | | | | | | | | | | | | | | | |
Db 1 gtgatagatgcgcagca 18

RESULT 2

US-60-234-049-123602
; Sequence 123602, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Escherichia coli
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234,049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123602
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-123602

Query Match 80.0%; Score 14.4; DB 62; Length 25;
Best Local Similarity 93.8%; Pred. No. 5e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 gtgatagatgcgcag 16
| | | | | | | | | | | | | | | |
Db 8 gtgatagtaagccgag 23

RESULT 3

US-09-954-427-357122
; Sequence 357122, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-09-954-427-357122

Query Match 74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 atagtgcgcagca 18
| | | | | | | | | | | | | | | |
Db 10 atagtgcgcagca 24

RESULT 4

US-09-954-427-357123
; Sequence 357123, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357123
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-09-954-427-357123

Query Match 74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 atagtgcgcagca 18
| | | | | | | | | | | | | | | |


```
Db      8 atagtattccgagca 22

RESULT 5
; Sequence 357134, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; DATABASE ACCESSION NUMBER: GenBank U77777
US-09-954-427-357134

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||
Db      6 atagtattccgagca 20

RESULT 6
US-09-954-429A-14687
; Sequence 14687, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 14687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-14689

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||
Db      10 atagtattccgagca 24

RESULT 9
US-09-956-584-141745
; Sequence 141745, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-141745

Query Match      74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 atagtattccgagca 18
        ||||||| |||||
Db      4 atagtattccgagca 18

RESULT 7
US-09-954-429A-14688
; Sequence 14688, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
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Db      2 atagtattccgagca 16
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; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-166-357122
RESULT 10
US-60-233-166-357122
; Sequence 357122, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-166-357122
Query Match      74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 atagtatgccgagca 18
||||||| |||||||
Db      10 atagtattccgagca 24
||||||| |||||||

RESULT 11
US-60-233-166-357123
; Sequence 357123, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357123
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-166-357123
Query Match      74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 atagtatgccgagca 18
||||||| |||||||
Db      10 atagtattccgagca 24
||||||| |||||||

RESULT 12
US-60-233-166-357134
; Sequence 357134, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17437
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-166-357134
Query Match      74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 atagtatgccgagca 18
||||||| |||||||
Db      8 atagtattccgagca 22
||||||| |||||||

RESULT 13
US-60-233-357-17436
; Sequence 17436, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17436
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-357-17436
Query Match      74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 atagtatgccgagca 18
||||||| |||||||
Db      10 atagtattccgagca 24
||||||| |||||||

RESULT 14
US-60-233-357-17437
; Sequence 17437, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17437
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-357-17437
Query Match      74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 atagtatgccgagca 18
||||||| |||||||
Db      10 atagtattccgagca 24
||||||| |||||||
```

; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-357-17437

Query Match 74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 atagtatgccgagca 18
| | | | | | | | | |
Db 8 atagtattccgagca 22

RESULT 15
US-60-233-357-17438
; Sequence 17438, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TITLE OF INVENTION: Neurobiology
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U77777
US-60-233-357-17438

Query Match 74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 atagtatgccgagca 18
| | | | | | | | | |
Db 6 atagtattccgagca 20

Search completed: October 12, 2002, 20:42:30
Job time: 16400 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:28 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-3
Perfect score: 18
Sequence: 1 gtgatatgtatgccgagca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-3
2	14.4	80.0	25	5	US-09-956-604-109679
3	12.2	67.8	25	5	US-09-396-196G-59455
4	12.2	67.8	25	5	US-09-396-196G-59456
5	12.2	67.8	25	5	US-09-396-196G-107073
6	11.8	65.6	16	1	PCT-US02-25943-62317
7	11.8	65.6	17	1	PCT-US02-25943-32519
8	11.8	65.6	18	1	PCT-US02-11683-26
9	11.8	65.6	18	7	US-10-122-013-26
10	11.8	65.6	23	5	US-09-803-876A-17
11	11.8	65.6	40	6	US-10-035-832-607
12	11.8	65.6	40	7	US-10-105-613-147
13	11.8	65.6	42	7	US-10-170-097-756
14	11.6	64.4	25	5	US-09-956-604-18296
15	11.4	63.3	15	1	PCT-US02-25940-6508
16	11.4	63.3	15	1	PCT-US02-25940-11096
17	11.4	63.3	17	1	PCT-US02-25943-32518
18	11.4	63.3	17	1	PCT-US02-25943-55833
19	11.4	63.3	18	1	PCT-US02-25940-129
20	11.4	63.3	20	1	PCT-US02-25940-6507
21	11.4	63.3	20	1	PCT-US02-25940-6509
22	11.4	63.3	22	1	PCT-US02-25943-52885
23	11.4	63.3	23	1	PCT-US02-25943-13010
24	11.4	63.3	25	5	US-09-956-604-129261
25	11.4	63.3	25	5	US-09-396-196G-3199

c 26	11.4	63.3	25	5	US-09-396-196G-3200	Sequence 3200, Ap
c 27	11.4	63.3	25	5	US-09-396-196G-84295	Sequence 84295, A
c 28	11.4	63.3	25	5	US-09-396-196G-84296	Sequence 84296, A
c 29	11.4	63.3	25	5	US-09-396-196G-84297	Sequence 84297, A
c 30	11.4	63.3	32	1	PCT-US02-25940-14492	Sequence 14492, A
c 31	11.4	63.3	34	1	PCT-US02-25943-33116	Sequence 33116, A
c 32	11.4	63.3	39	1	PCT-US02-25943-33117	Sequence 33117, A
c 33	11.2	62.2	20	7	US-10-128-560-85	Sequence 85, Appl
c 34	11.2	62.2	20	7	US-10-128-560-185	Sequence 185, Appl
c 35	11.2	62.2	25	5	US-09-956-604-95770	Sequence 95770, A
c 36	11.2	62.2	25	5	US-09-956-604-108981	Sequence 108981, A
c 37	11.2	62.2	25	5	US-09-956-604-113654	Sequence 113654, A
c 38	11.2	62.2	25	5	US-09-956-604-128604	Sequence 128604, A
c 39	11.2	62.2	25	5	US-09-396-196G-45766	Sequence 45766, A
c 40	11.2	62.2	25	5	US-09-396-196G-45767	Sequence 45767, A
c 41	11.2	62.2	25	6	US-10-215-112-12832	Sequence 12832, A
c 42	11.2	62.2	26	1	PCT-US02-25943-38378	Sequence 38378, A
c 43	11.2	62.2	34	7	US-10-078-113-155	Sequence 155, Appl
c 44	11.2	62.2	34	7	US-10-090-182A-155	Sequence 155, Appl
c 45	11.2	62.2	34	7	US-10-179-940-155	Sequence 155, Appl

ALIGNMENTS

RESULT 1
US-09-945-131-3
; Sequence 3, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945.131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-3

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.64; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 gtgatatgtatgccgagca 18
| | | | | | | | | | | | | | | | | |
Db 1 gtgatatgtatgccgagca 18

RESULT 2
US-09-956-604-109679
; Sequence 109679, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956.604
; CURRENT FILING DATE: 2001-09-19

```
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 109679
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-109679
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 gtgatagtatgccgag 16
    ||||| ||||| |||||
DB 8 gtgatagtaagccgag 23
```

```
RESULT 3
US-09-396-196G-59455/c
; Sequence 59455, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-59455
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```
Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 gtgatagtatgccgagc 17
    ||||| ||||| |||||
DB 24 GTGAGGATATGCCGAGC 8
```

```
RESULT 4
US-09-396-196G-59456/c
; Sequence 59456, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-59456
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```
Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 gtgatagtatgccgagc 17
    ||||| ||||| |||||
DB 21 GTGAGGATATGCCGAGC 5
```

```
RESULT 5
US-09-396-196G-107073/c
; Sequence 107073, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107073
```

```
Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 gtgatagtatgccgagc 17
    ||||| ||||| |||||
DB 20 GTAATAGTAGTGGGAGC 4
```

```
RESULT 6
PCT-US02-25943-62317/c
; Sequence 62317, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62317
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6082328)...(6082343)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 66
PCT-US02-25943-62317
```

```
Query Match      65.6%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 atagtatgccgagca 18
    ||||| ||||| |||||
DB 16 AGAGCATATGCCGAGCA 2
```

```
RESULT 7
PCT-US02-25943-32519/c
; Sequence 32519, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 32519
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3178057)...(3178073)
; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectronObjectNumber = 34846
PCT-US02-25943-32519

Query Match 65.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 atagtatgccgagca 18
Db 17 AGAGCATGCCCCAGCA 3

RESULT 8
PCT-US02-11683-26/c
; Sequence 26, Application PC/TUS0211683
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK ET AL
; TITLE OF INVENTION: NUCLEIC ACIDS FOR INHIBITING HAIRLESS PROTEIN EXPRESSION AND METH
; FILE REFERENCE: USE THEREOF
; CURRENT APPLICATION NUMBER: PCT/US02/11683
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIALSEQUENCE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: ANTISENSEOLIGONUCLEOTIDEDIRECTED AT HUMAN HAIRLESS
PCT-US02-11683-26

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gatagtatgccgagc 17
Db 15 GAGAGTATGCCAGC 1

RESULT 9
US-10-122-013-26/c
; Sequence 26, Application US/10122013
; GENERAL INFORMATION:
; APPLICANT: Christiano, Angela
; TITLE OF INVENTION: NUCLEIC ACIDS FOR INHIBITING HAIRLESS PROTEIN EXPRESSION AND METH
; FILE REFERENCE: USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/122,013
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIALSEQUENCE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: ANTISENSEOLIGONUCLEOTIDEDIRECTED AT HUMAN HAIRLESS
US-10-122-013-26

Query Match 65.6%; Score 11.8; DB 7; Length 18;
Best Local Similarity 86.7%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gatagtatgccgagc 17
Db 15 GAGAGTATGCCAGC 1

RESULT 10
US-09-803-676A-17
; Sequence 17, Application US/09803676A
; GENERAL INFORMATION:
; APPLICANT: Terry, L. I.
; APPLICANT: Chase, Kevin
; TITLE OF INVENTION: QUANTITATIVE TRAIT LOCI FOR INSECT RESISTANCE IN PLANTS
; FILE REFERENCE: 14-00
; CURRENT APPLICATION NUMBER: US/09/803,676A
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,439
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 17
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide Primer
US-09-803-676A-17

Query Match 65.6%; Score 11.8; DB 5; Length 23;
Best Local Similarity 86.7%; Pred. No. 3.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gtgatagtatgccga 15
Db 2 gtgacagtataccga 16

RESULT 11
US-10-035-832-607
; Sequence 607, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 607
; LENGTH: 40
; TYPE: DNA
```

; ORGANISM: Mus musculus
US-10-035-832-607

Query Match 65.6%; Score 11.8; DB 6; Length 40;
Best Local Similarity 86.7%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 gatagtatgccgagc 17
||||| |||||
Db 13 gatagtaagccgggc 27

RESULT 12
US-10-105-613-147
; Sequence 147, Application US/10105613
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER
; FILE REFERENCE: A-69959/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/105,613
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US/09/747,377
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 493
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-105-613-147

Query Match 65.6%; Score 11.8; DB 7; Length 40;
Best Local Similarity 86.7%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 gatagtatgccgagc 17
||||| |||||
Db 13 gatagtaagccgggc 27

RESULT 13
US-10-170-097-756
; Sequence 756, Application US/10170097
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pn
; SEQ ID NO 756
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele

; LOCATION: 24
; OTHER INFORMATION: 12-389-431 : polymorphic base C or T
US-10-170-097-756

Query Match 65.8%; Score 11.8; DB 7; Length 42;
Best Local Similarity 76.5%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 gtgatatgtatgccgagc 17
|:|:| ||||| |||||
Db 23 gygaaagatgtgtgagc 39

RESULT 14
US-09-956-604-18296/c
; Sequence 18296, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-18296

Query Match 64.4%; Score 11.6; DB 5; Length 25;
Best Local Similarity 77.8%; Pred. No. 5.1e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 gtgatatgtatgccgagca 18
| | ||||| |||||
Db 18 GGTCTAGTAGCCGAGCA 1

RESULT 15
PCT-US02-25940-6508
; Sequence 6508, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 6508
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (807312)...(807326)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 7
PCT-US02-25940-6508

Query Match 63.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 agtatgccgagca 18
|| ||||| |||||
Db 1 agtatgccgagca 13

Search completed: October 12, 2002, 17:27:29
Job time: 10804 sec

JOURNAL	PATENT: US 5814517-A 112 29-SEP-1998;
FEATURES	Location/Qualifiers
SOURCE	1..18
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BASE COUNT	4 a 4 c 4 g 6 t
ORIGIN	
Query Match	66.7%; Score 12; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 2.3e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 cggtacgtaagc 12
Db	17 CGTTACGTAAGC 6
RESULT	9
LOCUS	AR043743
DEFINITION	Sequence 113 from patent US 5814517.
ACCESSION	AR043743
VERSION	AR043743.1 GI:5964751
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Seidel,H.Martin., and Lamb,I.Peter.
TITLE	DNA spacer regulatory elements responsive to cytokines and methods for their use
JOURNAL	PATENT: US 5814517-A 113 29-SEP-1998;
FEATURES	Location/Qualifiers
SOURCE	1..18
/organism="unknown"	
BASE COUNT	6 a 4 c 4 g 4 t
ORIGIN	
Query Match	66.7%; Score 12; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 2.3e+04;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 cggtacgtaagc 12
Db	6 CGTTACGTAAGC 17
RESULT	10
LOCUS	AR063624
DEFINITION	Sequence 35 from patent US 5846715.
ACCESSION	AR063624
VERSION	AR063624.1 GI:5992932
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 31)
AUTHORS	Purcell,D.Francis.John., Russell,S.May. and McKenzie,I.Farquar.Campbell.
TITLE	CD46 variants
JOURNAL	PATENT: US 5846715-A 35 08-DEC-1998;
FEATURES	Location/Qualifiers
SOURCE	1..31
/organism="unknown"	
BASE COUNT	9 a 6 c 7 g 9 t
ORIGIN	
Query Match	65.6%; Score 11.8; DB 6; Length 31;
Best Local Similarity	86.7%; Pred. No. 3e+04;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 4 tacgtaagccttagga 18
   ||| ||| ||| ||| |||
Db 1 TAAGTAGGCCTAGGA 15

RESULT 11
AL8606/c
LOCUS          Al8606          42 bp      DNA          linear          PAT 26-JAN-1995
DEFINITION     H. sapiens CD46 exon 9 (STP C).
ACCESSION      Al8606
VERSION        Al8606.1 GI:513317
KEYWORDS       synthetic construct.
SOURCE          synthetic construct.
ORGANISM       artificial sequence.
REFERENCE      1 (bases 1 to 42)
AUTHORS        CD46 VARIANTS
TITLE          Patent: WO 9118097-A 25 28-NOV-1991;
JOURNAL        Location/Qualifiers
FEATURES       source
               1..42
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               <1..42
               /note="H. sapiens CD46 exon 9 (STP C)"
               /number=g
BASE COUNT     11 a 14 c 6 g 11 t
ORIGIN
               11 a 14 c 6 g 11 t

Query Match    65.6%; Score 11.8; DB 6; Length 42;
Best Local Similarity 86.7%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtaagccttagga 18
   ||| ||| ||| ||| |||
Db 16 TAAGTAGGCCTAGGA 2

RESULT 12
AR063615/c
LOCUS          AR063615          42 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION     Sequence 19 from patent US 5846715.
ACCESSION      AR063615
VERSION        AR063615.1 GI:5992923
KEYWORDS       Unknown.
SOURCE          Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 42)
AUTHORS        Purcell,D.Francis.John., Russell,S.May. and
               McKenzie,I.Farquar.Campbell.
TITLE          CD46 variants
JOURNAL        Patent: US 5846715-A 19 08-DEC-1998;
FEATURES       Location/Qualifiers
               source
               1..42
               /organism="unknown"
BASE COUNT     11 a 14 c 6 g 11 t
ORIGIN
               11 a 14 c 6 g 11 t

Query Match    65.6%; Score 11.8; DB 6; Length 42;
Best Local Similarity 86.7%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtaagccttagga 18
   ||| ||| ||| ||| |||
Db 16 TAAGTAGGCCTAGGA 2

RESULT 13
AX289339
LOCUS          AX289339          24 bp      DNA          linear          PAT 21-NOV-2001
DEFINITION     Sequence 1101 from Patent WO0179548.
ACCESSION      AX289339
VERSION        AX289339.1 GI:17051022
KEYWORDS       synthetic construct.
SOURCE          synthetic construct.
ORGANISM       artificial sequence.
REFERENCE      1 (sites)
AUTHORS        Barany,F., Zlrvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE          Method of designing addressable array for detection of nucleic acid
               sequence differences using ligase detection reaction
JOURNAL        Patent: WO 0179548-A 1101 25-OCT-2001;
               CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES       Location/Qualifiers
               source
               1..24
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="Hypothetical Probe Sequence"
BASE COUNT     5 a 8 c 5 g 6 t
ORIGIN
               5 a 8 c 5 g 6 t

Query Match    64.4%; Score 11.6; DB 6; Length 24;
Best Local Similarity 77.8%; Pred. NO. 4.1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
   ||||| ||| ||| |||
Db 1 CGTTACGGAATCCTTGCA 18

RESULT 14
ECORRG15
LOCUS          ECORRG15          38 bp      rRNA          linear          BCT 11-AUG-1995
DEFINITION     E.coli 23S ribosomal RNA, fragment J.
ACCESSION      K01121
VERSION        K01121.1 GI:174396
KEYWORDS       23S ribosomal RNA; ribosomal RNA.
SEGMENT        15 of 26
SOURCE          Escherichia coli rRNA.
ORGANISM       Escherichia coli
REFERENCE      1 (bases 1 to 38)
AUTHORS        Branlant,C., Krol,A., Machatt,M.A. and Ebel,J.P.
TITLE          Structural study of ribosomal 23 S RNA from Escherichia coli
JOURNAL        FEBS Lett. 107 (1), 177-181 (1979)
MEDLINE        80047286
COMMENT        See segment 1.
FEATURES       Location/Qualifiers
               source
               1..38
               /organism="Escherichia coli"
               /db_xref="taxon:562"
               <1..38
               /product="23S ribosomal RNA"
BASE COUNT     6 a 4 c 17 g 11 t
ORIGIN
               6 a 4 c 17 g 11 t

Query Match    64.4%; Score 11.6; DB 1; Length 38;
Best Local Similarity 77.8%; Pred. NO. 4.1e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
   ||||| ||| ||| |||
Db 18 CGTTCTGTAAGCCTGTGA 35

RESULT 15
E37995/c
LOCUS          E37995          42 bp      DNA          linear          PAT 31-JAN-2002
DEFINITION     Process for producing protein variant, process for constructing

```

protein variant library, and process for constructing protein
variant-encoding cDNA library.

ACCESSION E37995
VERSION E37995.1 GI:18626896
KEYWORDS JP 2000236880-A/13.
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 42)
AUTHORS Imamura,T., Asada,M., Suzuki,M., Oka,S. and Yoneda,A.
TITLE Process for producing protein variant, process for constructing
protein variant library, and process for constructing protein
variant-encoding cDNA library
JOURNAL Patent: JP 2000236880-A 13 05-SEP-2000;
COMMENT AGENCY OF IND SCIENCE & TECHNOL
OS Artificial Sequence
PN JP 2000236880-A/13
PD 05-SEP-2000
PF 19-FEB-1999 JP 1999041538
PR
PI TORU IMAMURA,MASAHIRO ASADA,MAKOTO SUZUKI,SHUICHI OKA, PI
ATSUKO YONEDA
PC C12N15/09,C07K14/475,C12N5/10,C12P21/02//C12N15/09,C12R1:91),
PC (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
CC (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
FT
FH Key Location/Qualifiers
FT source 1..42
/organism='Artificial Sequence'.

FEATURES
source
1..42
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 9 a 16 c 7 g 10 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 42;
Best Local Similarity 77.8%; Pred. No. 4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 cgttacgtaagcctagga 18
||| ||||| |||
Db 25 CGTAACTTAAGCCGGGA 8

Search completed: October 12, 2002, 16:51:16
Job time: 8891 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:02 ; Search time 792.17 seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-4

Perfect score: 18

Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
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- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
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- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	21	AA13835
2	13.2	73.3	26	16	AAQ9868
3	12.8	71.1	34	21	AAA60557
4	12.2	67.8	18	21	AAA60553
5	12.2	67.8	25	16	AAQ99545
6	12.2	67.8	38	21	AACT3635
7	12	66.7	18	19	AAV56953
8	12	66.7	18	19	AAV56954
9	11.8	65.6	31	12	AAQ14923

10	11.8	65.6	50	22	AA133677	Human SNP oligonuc
11	11.6	64.4	24	24	ABI84598	Capture oligonucle
12	11.6	64.4	24	24	ABI84599	Capture oligonucle
13	11.6	64.4	42	21	AAQ66117	PCR primer #3n-IR
14	11.6	64.4	50	17	AAQ35090	Oligonucleotide wh
15	11.6	64.4	50	17	AAAT1692	Oligonucleotide co
16	11.6	64.4	50	17	AAAT37107	Oligonucleotide ha
17	11.4	63.3	22	18	AAAT84535	Serotonin transpor
18	11.4	63.3	27	18	AAAT91263	GBV hepatitis viru
19	11.4	63.3	36	10	AAAT90552	Tissue plasminogen
20	11.4	63.3	47	18	AAAT74123	AACT-K391T/K396T d
21	11.2	62.2	20	22	AAQ59668	HBV surface antige
22	11.2	62.2	25	16	AAQ92995	Pre-invasive human
23	11.2	62.2	25	19	AAAT19232	Primer ON6 to ampl
24	11.2	62.2	27	14	AAQ43337	Sequence of PCR pr
25	11.2	62.2	27	21	AAZ55159	Neisseria species
26	11.2	62.2	28	17	AAAT33625	Primer for murine
27	11.2	62.2	29	19	AAV44042	Mouse bFGF recepto
28	11.2	62.2	32	22	AAAT7813	CREB probe derived
29	11.2	62.2	34	17	AAAT31729	Escherichia coli c
30	11.2	62.2	35	14	AAQ43340	Sequence of PCR pr
31	11.2	62.2	37	19	AAV04084	Somatostatin gene
32	11.2	62.2	39	18	AAAT87127	IFN-gamma 2'F RNA
33	11.2	62.2	40	20	AAAX90938	Oligonucleotide cr
34	11.2	62.2	40	21	AAAX92339	Hepatitis B virus
35	11.2	62.2	44	20	AAAX90937	Oligonucleotide cr
36	11.2	62.2	45	22	AAQ9526	Human IL-17D hybri
37	11.2	62.2	47	19	AAV30386	Oligomer p47rg24 u
38	11.2	62.2	50	21	AAZ91705	P. microspora telo
39	11.2	62.2	50	21	AAZ91716	P. microspora telo
40	11.2	62.2	50	22	AAAT74731	Human silent SNP c
41	11.2	62.2	50	22	AAAT74733	Human silent SNP c
42	11	61.1	20	20	AAZ02278	PCR primer used to
43	11	61.1	27	22	AAQ9842	Primer for detecti
44	11	61.1	30	17	AAAT33118	Primer 2A for ampl
45	10.8	60.0	16	18	AAAT92448	TAT system oligonu

ALIGNMENTS

RESULT 1
ID AA13835 standard; DNA; 18 BP.

XX AA13835;

AC AA13835;

XX 27-JUL-2000 (first entry)

DT Murine PDGFR-beta scrambled control oligonucleotide SEQ ID NO:4.

DE Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
recurrent stenosis; cardiovascular injury; ss.

XX Mus sp.

XX Key Location/Qualifiers

FT modified_base 1..18

FT /*tag= a

FT /*note= "phosphorothioate linkages"

XX CA2228977-A1.

XX 07-MAY-1999.

XX 03-FEB-1998; 98CA-2228977.

XX 07-NOV-1997; 97CA-2215360.

XX (EDEL/) EDELMAN E R.

XX (ROSE/) ROSENBERG R D.

XX (SIRO/) SIROIS M G.

KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
 XX Unidentified.
 OS
 XX
 PN W0200058516-A2.
 XX
 PD 05-OCT-2000.
 XX
 XX 27-MAR-2000; 2000WO-US08069.
 XX
 XX 26-MAR-1999; 99US-0126473.
 PR
 PR 23-JUN-1999; 99US-0140359.
 XX
 XX (WHEATHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 XX
 XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
 PI Ryder T, Sklar P;
 XX WPI; 2000-656171/63.
 DR
 XX
 XX Universal array of oligonucleotides tags attached to a solid substrate
 PT along with locus-specific tagged oligonucleotides useful in genotyping
 PT using single base extension reactions -
 XX
 XX Example 7; Page 63; 83pp; English.
 PS
 XX The present invention relates to an oligonucleotide array comprising
 CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
 CC array is useful for genotyping a nucleic acid sample at one or more loci
 CC via single base extension (SBE) reactions. A pair of primers is used to
 CC amplify a polymorphic locus in a sample e.g. a single nucleotide
 CC polymorphism (SNP). The amplified nucleic acid product is then used as a
 CC template in a SBE reaction with an extension primer. The present sequence
 CC is one such SBE reaction primer used in the method of the present
 CC invention. The SBE reaction products are used to form the oligonucleotide
 CC array.
 XX
 XX Sequence 38 BP; 8 A; 10 C; 10 G; 10 T; 0 other;

Query Match 67.88; Score 12.2; DB 21; Length 38;
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgttaagcctagg 17
 |||||
 Db 7 cgttacgtgagctctcgg 23

RESULT 7
 AAV56953/C
 ID AAV56953 standard; DNA; 18 BP.
 XX
 AC AAV56953;
 XX
 XX 02-DEC-1998 (first entry)
 XX
 XX Regulatory element containing oligonucleotide #112.
 DE
 XX Cytokine-responsive regulatory; primer; promoter; detection; isolation;
 KW transcriptional control; STAT protein; screening; agonist; ss.
 KW
 XX Synthetic.
 OS
 XX US5814517-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 27-MAR-1995; 95US-0410779.
 PF
 XX 27-MAR-1995; 95US-0410779.
 PR
 PR 14-APR-1994; 94US-0228935.

XX (LIGA-) LIGAND PHARM INC.
 PA
 XX Lamb IP, Seidel HM;
 PI
 XX WPI; 1998-541763/46.
 DR
 XX
 XX DNA constructs containing cytokine-responsive regulatory elements -
 PT useful in assays for transcription-regulating proteins or gene
 PT transcription agonists or antagonists
 XX
 XX Example 2; Column 27-28; 58pp; English.
 PS
 XX AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
 CC production of constructs comprising a cytokine-responsive regulatory
 CC element linked to a promoter which is linked to a heterologous coding
 CC sequence so that the coding sequence is under the transcriptional
 CC control of the regulatory element and the promoter, where the regulatory
 CC element has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and
 CC TTCNVTAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be
 CC used to detect or isolate transcription-regulating proteins, e.g. STAT
 CC proteins, in a sample by contacting the sample with the construct so that
 CC the protein binds to the regulatory element, and detecting or separating
 CC the resulting complex. The cells can be used in screening assays for
 CC agonists of gene transcription, in which the level of expression of the
 CC coding sequence is measured in the presence and absence of a test
 CC compound or in the presence of the corresponding cytokine.
 XX
 XX Sequence 18 BP; 4 A; 4 C; 4 G; 6 T; 0 other;
 SQ
 Query Match 66.7%; Score 12; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 cgttacgttaagc 12
 |||||
 Db 17 CGTTACGTAAGC 6
 RESULT 8
 AAV56954
 ID AAV56954 standard; DNA; 18 BP.
 XX
 AC AAV56954;
 XX
 XX 02-DEC-1998 (first entry)
 DT
 XX
 XX Regulatory element containing oligonucleotide #113.
 DE
 XX Cytokine-responsive regulatory; primer; promoter; detection; isolation;
 KW transcriptional control; STAT protein; screening; agonist; ss.
 KW
 XX Synthetic.
 OS
 XX US5814517-A.
 PN
 XX 29-SEP-1998.
 PD
 XX 27-MAR-1995; 95US-0410779.
 PF
 XX 27-MAR-1995; 95US-0410779.
 PR
 PR 14-APR-1994; 94US-0228935.
 XX
 XX (LIGA-) LIGAND PHARM INC.
 PA
 XX Lamb IP, Seidel HM;
 PI
 XX WPI; 1998-541763/46.
 DR
 XX
 XX DNA constructs containing cytokine-responsive regulatory elements -
 PT useful in assays for transcription-regulating proteins or gene
 PT transcription agonists or antagonists

XX Example 2; Column 27-28; 58pp; English.
 PS
 CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
 CC production of constructs comprising a cytokine-responsive regulatory
 CC element linked to a promoter which is linked to a heterologous coding
 CC sequence so that the coding sequence is under the transcriptional
 CC control of the regulatory element and the promoter, where the regulatory
 CC element has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and
 CC TTCNVTAA where N is A, T, C or G, and y = 3 or 4. The constructs can be
 CC used to detect or isolate transcription-regulating proteins, e.g. SPAT
 CC proteins, in a sample by contacting the sample with the construct so that
 CC the protein binds to the regulatory element, and detecting or separating
 CC the resulting complex. The cells can be used in screening assays for
 CC agonists of gene transcription, in which the level of expression of the
 CC coding sequence is measured in the presence and absence of a test
 CC compound or in the presence of the corresponding cytokine.
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 other;

Query Match 66.7%; Score 12; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagc 12
 |||||
 Db 6 cgttacgtaagc 17

RESULT 9
 AAQ14923
 ID AAQ14923 standard; DNA; 31 BP.
 XX
 AC AAQ14923;
 XX
 DT 17-MAR-1992 (first entry)
 DE
 DE CD46 exon 6-9 probe.
 XX
 KW Alternative splicing; splice variant; membrane cofactor protein;
 KW MCP; ss.
 XX
 OS Synthetic.
 XX
 PN WO9118097-A.
 XX
 XX 28-NOV-1991.
 PD
 XX
 PF 10-MAY-1991; 91WO-AU00199.
 XX
 PR 11-MAY-1990; 90AU-0000133.
 XX
 PA (UYME-) UNIV MELBOURNE.
 XX
 PI Purcell DFJ, Russell SM, McKenzie JFC;
 XX
 DR WPI; 1991-369251/50.
 XX
 PT New CD46 membrane cofactor protein variants - useful as probes
 PT to identify CD46 isoforms and for diagnosing spontaneous
 PT abortion, inhibiting immuno:response and treating leukaemia
 XX
 PS Disclosure; Page 22; 77pp; English.
 XX
 CC The probes represented in AAQ14921-25 and AAQ15211-12 were used to
 CC determine the tissue distribution of alternatively spliced CD46
 CC RNA transcripts.
 CC
 CC See also AAQ14915-25, AAQ15211-12 and AAR15457-59.
 XX
 SQ Sequence 31 BP; 9 A; 6 C; 7 G; 9 T; 0 other;

Query Match 65.6%; Score 11.8; DB 12; Length 31;
 Best Local Similarity 86.7%; Pred. No. 2.1e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 tacgtaagcctagga 18
 |||||
 Db 1 taagttaggcctagga 15

RESULT 10
 AAL33677
 ID AAL33677 standard; DNA; 50 BP.
 XX
 AC AAL33677;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #6885.

XX Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

PN 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

XX Claim 1; Page 3351; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

XX Sequence 50 BP; 11 A; 9 C; 17 G; 13 T; 0 other;

Query Match 65.6%; Score 11.8; DB 22; Length 50;
 Best Local Similarity 86.7%; Pred. No. 2.2e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtacgccttagga 18
 ||| ||| ||| ||| |||

Db 8 taagtgccttagga 22

RESULT 11
ABI84598
ID ABI84598 standard; DNA; 24 BP.
XX
AC ABI84598;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1101 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Brucella
CC melitensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying (if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 5 A; 8 C; 5 G; 6 T; 0 other;

Query Match 64.4%; Score 11.6; DB 24; Length 24;

Query Match 64.4%; Score 11.6; DB 24; Length 24;
 Best Local Similarity 77.8%; Pred. No. 2.7e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctaggaa 18
 DB 24 CGTTACGGAATCCTTGCA 7

RESULT 13
 AAC66117/C
 ID AAC66117 standard; DNA; 42 BP.
 XX
 AC AAC66117;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE PCR primer #3n+IR used in mutant protein library construction.
 KW Human; fibroblast growth factor; FGF; mutant protein library preparation;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN JP2000236880-A.
 XX
 PD 05-SEP-2000.
 XX
 PF 19-FEB-1999; 99JP-0041538.
 XX
 PR 19-FEB-1999; 99JP-0041538.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 XX
 DR WPI; 2000-658507/64.
 XX
 PT Production of a mutant protein, preparation of a mutant protein library
 and preparation of a cDNA library encoding a mutant protein -
 XX
 PS Examples; Page 8; 36pp; Japanese.
 XX
 CC This invention relates to the preparation of a cDNA library encoding a
 mutant in which an amino acid or a peptide is introduced to a random site
 on the primary structure of a protein. The method comprises recombining
 cDNA encoding a protein to a cyclic plasmid and cleaving the cyclic
 plasmid at one random site and introducing a cDNA encoding an amino acid
 or a peptide at the cleaved site. The method is used to optimise protein
 CC mutation introduction rates. The present sequence represents a PCR primer
 used in an illustration of the method of the invention.
 XX
 SQ Sequence 42 BP; 9 A; 16 C; 7 G; 10 T; 0 other;

Query Match 64.4%; Score 11.6; DB 21; Length 42;
 Best Local Similarity 77.8%; Pred. No. 2.8e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctaggaa 18
 DB 25 CGTAACTTAAGCCCGGA 8

RESULT 14
 AAX35090
 ID AAX35090 standard; cDNA; 50 BP.
 XX
 AC AAX35090;
 XX
 DT 01-JUL-1999 (first entry)
 XX
 DE Oligonucleotide which is internally functionalized.
 XX
 KW Internucleotide linkage; N-aminoalkyl phosphoramidate;

aminoalkyl group; internally labelled oligonucleotide analogue; ss.
 XX Synthetic.
 OS
 PN US5563253-A.
 XX
 PD 08-OCT-1996.
 XX
 PF 03-MAR-1994; 94US-0206175.
 XX
 PR 03-MAR-1994; 94US-0206175.
 PR 08-MAR-1990; 90US-0490481.
 XX
 PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.
 XX
 PI Agrawal S, Tang J;
 XX
 DR WPI; 1996-464214/46.
 XX
 PT Oligo:nucleotide analogues for internal labelling - containing
 aminoalkyl phosphoramidate inter:nucleotide linkages
 XX
 PS Example 1; Columns 7-8; 14pp; English.
 XX
 CC Oligonucleotides AAX35084-92 exemplify the invention. They represents
 oligonucleotide analogues which comprise a linear chain of 17-50
 nucleotides with at least one internucleotide linkage being an
 N-aminoalkyl phosphoramidate group. The aminoalkyl group can be
 labelled non-radioactively, e.g. with biotin, fluorescein or rhodamine,
 CC to provide internally labelled oligonucleotide analogues useful in
 research or in the diagnosis and treatment of diseases and conditions
 CC of interest.
 XX
 SQ Sequence 50 BP; 13 A; 11 C; 15 G; 11 T; 0 other;

Query Match 64.4%; Score 11.6; DB 17; Length 50;
 Best Local Similarity 77.8%; Pred. No. 2.9e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctaggaa 18
 DB 1 cgtacgtaagcctaggaa 18

RESULT 15
 AAT41692
 ID AAT41692 standard; DNA; 50 BP.
 XX
 AC AAT41692;
 XX
 DT 05-DEC-1996 (first entry)
 XX
 DE Oligonucleotide containing aminoalkylphosphotriester linkage.
 XX
 KW aminoalkylphosphotriester; internally functionalised; linkage;
 KW diagnosis; non-radioactively labelled; ss.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT misc_difference 1..50
 FT /*tag= a
 FT /note= "at least one linkage along the chain is an
 aminoalkylphosphotriester residue of
 structure -Nu2-O-P(O)[O(CH2)nNH2]-O-Nu1-
 (where n is 2-6 and Nu1 and Nu2 are the
 adjacent nucleosides) to which a
 non-radioactive label can be attached"

XX
 PN US5541305-A.
 XX
 PD 30-JUL-1996.

```
XX 16-DEC-1994; 94US-0357666.
XX
XX 03-MAR-1994; 94US-0206175.
XX 08-MAR-1990; 90US-0490481.
XX 16-DEC-1994; 94US-0357666.
XX
XX (WORC-) WORCESTER FOUND BIOMEDICAL RES.
XX
XX Agrawal S, Tang J;
XX WPI; 1996-362016/36.
XX
XX New oligo:nucleotide derivs. - having aminoalkyl:phospho:tri:ester
XX inter:nucleoside linkage which can be labelled or functionalised
XX
XX Examples; Column 8; 14pp; English.
XX
XX The invention relates to a compound consisting of 5-50 covalently linked
XX nucleosides in which at least one linkage between the nucleosides is
XX through an aminoalkyl phosphotriester residue having the formula
XX -Nu2-O-P(O)[O(CH2)nNH2]-O-Nu1-, where n is 2-6 and Nu1 and Nu2 are
XX those nucleosides adjacent to the residue. The amino group of the
XX modified linkage can be used to attach a non-radioactive label such as
XX biotin, fluorescein or rhodamine or their derivatives, so that the label
XX is attached at a predetermined position. The non-radioactively labelled
XX compound is useful in research and in the diagnosis and treatment of
XX diseases and conditions of interest. The present sequence is a specific
XX example of an oligonucleotide which incorporates the modified linkage.
XX
XX Sequence 50 BP; 13 A; 11 C; 15 G; 11 T; 0 other;
SQ
```

Query Match 64.4%; Score 11.6; DB 17; Length 50;
Best Local Similarity 77.8%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Oy 1 cgttacgtaagcctagga 18
   ||| |||| |||||
Db 1 cgatgcgtaggcctagaa 18
```

Search completed: October 12, 2002, 17:08:03
Job time: 9748 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:36 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-4

Perfect score: 18

Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12.8	71.1	20	4	US-09-593-711A-133
c 2	12.2	67.8	25	4	US-08-339-214-101
c 3	12	66.7	18	1	US-08-410-779B-112
c 4	12	66.7	18	1	US-08-410-779B-113
c 5	12	66.7	18	5	PCT-US95-04477-112
c 6	12	66.7	18	5	PCT-US95-04477-113
c 7	11.8	65.6	19	1	US-08-623-195-19
c 8	11.8	65.6	31	2	US-08-528-057-35
c 9	11.8	65.6	42	2	US-08-528-057-19
c 10	11.6	64.4	50	1	US-08-357-399-10
c 11	11.6	64.4	50	1	US-08-357-666-10
c 12	11.6	64.4	50	1	US-08-206-175-10
c 13	11.4	63.3	22	4	US-09-043-507-4
c 14	11.4	63.3	31	3	US-08-542-051-39
c 15	11.4	63.3	35	3	US-08-542-051-37
c 16	11.4	63.3	45	3	US-08-860-368B-8
c 17	11.4	63.3	47	1	US-08-435-480-7
c 18	11.2	62.2	20	4	US-09-593-711A-36
c 19	11.2	62.2	25	1	US-08-182-961B-15
c 20	11.2	62.2	25	4	US-09-007-678B-15
c 21	11.2	62.2	27	2	US-08-244-434-13
c 22	11.2	62.2	29	1	US-07-631-717A-2
c 23	11.2	62.2	29	1	US-08-306-255-5
c 24	11.2	62.2	29	1	US-08-166-717B-2
c 25	11.2	62.2	32	4	US-09-215-098-1
c 26	11.2	62.2	34	2	US-08-343-923-2
c 27	11.2	62.2	35	2	US-08-244-434-12

c 28	11.2	62.2	35	2	US-08-244-434-16	Sequence 16, Appl
c 29	11.2	62.2	37	4	US-09-025-769B-112	Sequence 112, App
c 30	11.2	62.2	40	2	US-09-130-114-18	Sequence 18, Appl
c 31	11.2	62.2	44	2	US-09-130-114-17	Sequence 17, Appl
c 32	11	61.1	21	2	US-08-855-429-8	Sequence 8, Appl
c 33	11	61.1	30	2	US-08-396-927A-3	Sequence 3, Appl
c 34	10.8	60.0	16	4	US-09-156-828B-24	Sequence 24, Appl
c 35	10.8	60.0	20	1	US-07-906-930E-20	Sequence 20, Appl
c 36	10.8	60.0	20	3	US-08-574-396-40	Sequence 40, Appl
c 37	10.8	60.0	20	3	US-08-310-259B-14	Sequence 14, Appl
c 38	10.8	60.0	20	4	US-08-973-568-40	Sequence 40, Appl
c 39	10.8	60.0	21	1	US-08-093-741-29	Sequence 29, Appl
c 40	10.8	60.0	21	1	US-08-720-012-29	Sequence 29, Appl
c 41	10.8	60.0	21	4	US-09-156-828B-22	Sequence 22, Appl
c 42	10.8	60.0	22	3	US-08-477-934-27	Sequence 27, Appl
c 43	10.8	60.0	29	1	US-08-093-741-30	Sequence 30, Appl
c 44	10.8	60.0	29	1	US-08-720-012-30	Sequence 30, Appl
c 45	10.8	60.0	30	2	US-08-528-057-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-593-711A-133/c
; Sequence 133, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RYS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-711A-133

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 68;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gttacgtaagcctagg 17
Db 17 GTTACGTAGCGCTCGG 2
||||| ||||| ||

RESULT 2

US-08-339-214-101
; Sequence 101, Application US/08339214
; Patent No. 6348334
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigikazu
; APPLICANT: Suda, Takashi
; APPLICANT: Takahashi, Tomoniro
; APPLICANT: Nakamura, No. 634833410
; TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
; TITLE OF INVENTION: Encoding the Same
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,214
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-139P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sense primer 20"
; ANTI-SENSE: NO
; US-08-339-214-101

Query Match 67.8%; Score 12.2; DB 4; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gttacgtaaagccctagga 18
||||| ||||| |||||
Db 5 GTTACCAGGCCAAGGA 21

RESULT 3
US-08-410-779B-112/c
; Sequence 112, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906

; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-410-779B-112

Query Match 66.7%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cgttacgtaagc 12
||||| ||||| |||||
Db 17 CGTTACGTAAGC 6

RESULT 4
US-08-410-779B-113
; Sequence 113, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-410-779B-113

Query Match 66.7%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagc 12
|||||
Db 6 CGTTACGTAAGC 17

RESULT 5
PCT-US95-04477-112/c
; Sequence 112, Application PC/TUS9504477
; GENERAL INFORMATION:
; APPLICANT: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
; TITLE OF INVENTION: 165
; NUMBER OF SEQUENCES: 165
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; SYNTHETIC DNA"
PCT-US95-04477-112

Query Match 66.7%; Score 12; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagc 12
|||||
Db 17 CGTTACGTAAGC 6

RESULT 6
PCT-US95-04477-113
; Sequence 113, Application PC/TUS9504477
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 165
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; SYNTHETIC DNA"
PCT-US95-04477-113

Query Match 66.7%; Score 12; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttacgtaagc 12
|||||
Db 6 CGTTACGTAAGC 17

RESULT 7
US-08-623-195-19/G
; Sequence 19, Application US/08623195
; Patent No. 5759810
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITO, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,195
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 71033/1995
; FILING DATE: 29-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 029430-293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-623-195-19

Query Match 65.6%; Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 tacgtaagcctagga 18
|||||
Db 15 TACTTAAGCCAAGGA 1

RESULT 8
US-08-528-057-35
; Sequence 35, Application US/08528057

Patent No. 5846715
GENERAL INFORMATION:
APPLICANT: PURCELL, Damian F. J.
APPLICANT: RUSSELL, Sarah M.
APPLICANT: MCKENZIE, Ian F. C.
TITLE OF INVENTION: CD46 VARIANTS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/528.057
FILING DATE: 10-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK0133/90
FILING DATE: 11-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17227/112 DACO
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: exons 6-9
US-08-528-057-35

Query Match 65.6%; Score 11.8; DB 2; Length 31;
Best Local Similarity 86.7%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtagccttagga 18
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Db 1 TAAAGTAGCCTTAGGA 15

RESULT 9
US-08-528-057-19/c
Sequence 19, Application US/08528057
Patent No. 5846715
GENERAL INFORMATION:
APPLICANT: PURCELL, Damian F. J.
APPLICANT: RUSSELL, Sarah M.
APPLICANT: MCKENZIE, Ian F. C.
TITLE OF INVENTION: CD46 VARIANTS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528.057
FILING DATE: CONCURRENTLY HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961.686
FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00199
FILING DATE: 10-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK0133/90
FILING DATE: 11-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17227/112 DACO
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: exon 9
US-08-528-057-19

Query Match 65.6%; Score 11.8; DB 2; Length 42;
Best Local Similarity 86.7%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tacgtagccttagga 18
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Db 16 TAAAGTAGCCTTAGGA 2

RESULT 10
US-08-357-399-10
Sequence 10, Application US/08357399
Patent No. 5536821
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
APPLICANT: Tang, Jin-Yan
TITLE OF INVENTION: Site-Specific Functionalization of
TITLE OF INVENTION: Oligodeoxynucleotides for
TITLE OF INVENTION: No. 5536821-Radioactive Labelling
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357.399

; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206175
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-014CPDV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-357-399-10

Query Match 64.4%; Score 11.6; DB 1; Length 50;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
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Db 1 CGATGCGTAGGCGCTAGAA 18

RESULT 11
US-08-357-666-10
; Sequence 10, Application US/08357666
; Patent No. 5541306
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; APPLICANT: Tang, Jin-Yan
; TITLE OF INVENTION: Site-Specific Functionalization of
; TITLE OF INVENTION: Oligodeoxynucleotides for
; TITLE OF INVENTION: No. 5541306-Radioactive Labelling
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,666
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206175
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-014CPDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-357-666-10

Query Match 64.4%; Score 11.6; DB 1; Length 50;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
||| ||||| ||||| |
Db 1 CGATGCGTAGGCGCTAGAA 18

RESULT 12
US-08-206-175-10
; Sequence 10, Application US/08206175
; Patent No. 5563253
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir and
; APPLICANT: Jin-Yan Tang
; TITLE OF INVENTION: Site-Specific Functionalization of
; TITLE OF INVENTION: Oligodeoxynucleotides for
; TITLE OF INVENTION: No. 5563253-Radioactive Labelling
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,175
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-014 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-206-175-10

Query Match 64.4%; Score 11.6; DB 1; Length 50;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctagga 18
||| ||||| ||||| |
Db 1 CGATGCGTAGGCGCTAGAA 18

RESULT 13
US-09-043-507-4/c
; Sequence 4, Application US/090433507
; Patent No. 6165716
; GENERAL INFORMATION:
; APPLICANT: BATTERSBY, SHARON
; APPLICANT: FINK, GEORGE
; APPLICANT: GOODWIN, GUY MANNING
; APPLICANT: HARMAR, ANTHONY JOHN
; APPLICANT: OGILVIE, ALAN DAVID
; APPLICANT: SMITH, CHRISTOPHER
; TITLE OF INVENTION: SCREENING FOR DISORDERS OF
; TITLE OF INVENTION: SEROTONERGIC DYSFUNCTION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,507
; FILING DATE: 23-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/02360
; FILING DATE: 23-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: RATNER, ALLAN
; REGISTRATION NUMBER: 19,717
; REFERENCE/DOCKET NUMBER: MUR-7060
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-043-507-4

Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 cgttaagcctagg 18
||| ||| ||| |||
Db 16 CGTAAGACTAGGA 4

RESULT 14
US-08-542-051-39
; Sequence 39, Application US/08542051F
; Patent No. 6004782
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; APPLICANT: McPherson, David T.
; APPLICANT: Urry, Dan W.
; APPLICANT: Xu, Jie
; TITLE OF INVENTION: Hyperexpression of Bioelastic Polypeptides
; FILE REFERENCE: BERL-018/01US
; CURRENT APPLICATION NUMBER: US/08/542,051F
; CURRENT FILING DATE: 1995-10-13

; EARLIER APPLICATION NUMBER: 08/423,642
; EARLIER FILING DATE: 1995-04-14
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-08-542-051-39

Query Match 63.3%; Score 11.4; DB 3; Length 31;
Best Local Similarity 92.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 acgtaagcctagg 17
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Db 17 acttaagcctagg 29

RESULT 15
US-08-542-051-37
; Sequence 37, Application US/08542051F
; Patent No. 6004782
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; APPLICANT: McPherson, David T.
; APPLICANT: Urry, Dan W.
; APPLICANT: Xu, Jie
; TITLE OF INVENTION: Hyperexpression of Bioelastic Polypeptides
; FILE REFERENCE: BERL-018/01US
; CURRENT APPLICATION NUMBER: US/08/542,051F
; CURRENT FILING DATE: 1995-10-13
; EARLIER APPLICATION NUMBER: 08/423,642
; EARLIER FILING DATE: 1995-04-14
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-08-542-051-37

Query Match 63.3%; Score 11.4; DB 3; Length 35;
Best Local Similarity 92.3%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 acgtaagcctagg 17
||| ||| ||| |||
Db 21 acttaagcctagg 33

Search completed: October 12, 2002, 16:54:36
Job time: 8991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:30 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-4

Perfect score: 18

Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 38: /cgn2_6/ptodata/2/pna/US101_COMB.seq.*
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- 41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq.*
- 42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq.*
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- 73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	14.4	80.0	25	74	US-60-353-987-681647	Sequence 681647,
3	13.8	76.7	25	62	US-60-232-638-76423	Sequence 76423, A
4	13.8	76.7	25	74	US-60-353-987-755566	Sequence 755566,
5	13.8	76.7	25	74	US-60-353-987-755567	Sequence 755567,
6	13.8	76.7	25	74	US-60-353-987-755568	Sequence 755568,
c	13.4	74.4	25	35	US-09-954-427-408320	Sequence 408320,
c	13.4	74.4	25	62	US-60-233-166-408320	Sequence 408320,
c	13.2	73.3	25	35	US-09-956-584-493346	Sequence 493346,
10	13.2	73.3	25	62	US-60-233-620-86428	Sequence 86428, A
11	13.2	73.3	25	62	US-60-233-620-86434	Sequence 86434, A
12	13.2	73.3	25	62	US-60-234-017-481562	Sequence 481562,
13	13.2	73.3	25	74	US-60-353-987-21692	Sequence 21692, A
14	13.2	73.3	25	74	US-60-353-987-104566	Sequence 104566,
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15	13.2	73.3	25	74	US-60-353-987-831824	Sequence 831824,
16	13.2	73.3	25	74	US-60-353-987-831824	Sequence 831824,
17	13.2	73.3	26	1	PCT-US94-12505-10	Sequence 10, Appl
18	13.2	73.3	26	5	US-08-142-124-10	Sequence 10, Appl
19	13.2	73.3	26	15	US-09-114-911-10	Sequence 10, Appl
20	13	72.2	25	74	US-60-353-987-506710	Sequence 506710,
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c	12.8	71.1	25	62	US-60-234-049-20336	Sequence 20336, A
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c	12.8	71.1	25	74	US-60-353-987-219543	Sequence 219543,
c	12.8	71.1	25	74	US-60-353-987-219780	Sequence 219780,
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c	12.8	71.1	25	74	US-60-353-987-533824	Sequence 533824,

c 32 12.8 71.1 25 74 US-60-353-987-533825, Sequence 533825,
c 33 12.8 71.1 25 74 US-60-353-987-681648, Sequence 681648,
c 34 12.8 71.1 25 74 US-60-353-987-733622, Sequence 733622,
c 35 12.8 71.1 25 74 US-60-353-987-782764, Sequence 782764,
c 36 12.8 71.1 34 16 US-09-254-326-4, Sequence 4, Appl1
c 37 12.8 71.1 34 32 US-09-856-652-6, Sequence 6, Appl1
c 38 12.8 71.1 47 60 US-60-216-745-2749, Sequence 2749, Ap
c 39 12.4 68.9 25 26 US-09-660-220-73594, Sequence 73594, A
c 40 12.4 68.9 25 35 US-09-954-427-56195, Sequence 56195, A
c 41 12.4 68.9 25 35 US-09-954-427-56196, Sequence 56196, A
c 42 12.4 68.9 25 35 US-09-954-427-288140, Sequence 288140,
c 43 12.4 68.9 25 35 US-09-956-584-262356, Sequence 262356,
c 44 12.4 68.9 25 35 US-09-956-584-363799, Sequence 363799,
c 45 12.4 68.9 25 62 US-60-232-638-30976, Sequence 30976, A

ALIGNMENTS

RESULT 1
US-09-241-561-4
; Sequence 4, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-4

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 18
|||||
Db 1 cgttacgtaagcctagg 18

RESULT 2
US-60-353-987-681647/c
; Sequence 681647, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 681647
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-681647

Query Match 80.0%; Score 14.4; DB 74; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttacgtaagcctagg 18
|||||
Db 24 TTACGTAAGCCTAGAA 9

RESULT 3
US-60-232-638-76423
; Sequence 76423, Application US/60232638
; GENERAL INFORMATION:
; APPLICANT: MITTMANN
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3110
; CURRENT APPLICATION NUMBER: US/60/232,638
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76423
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cervisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YHR106W
US-60-232-638-76423

Query Match 76.7%; Score 13.8; DB 62; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 8 cgttacgtaggcctgg 24

RESULT 4
US-60-353-987-755566
; Sequence 755566, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 755566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-755566

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 3 cgttacgtaagcctagg 19

RESULT 5
US-60-353-987-755567
; Sequence 755567, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: MITTMANN, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33

; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353.987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 755567
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-60-353-987-755567

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 3 cgttacgtaagcaggg 19
|||||

RESULT 6
US-60-353-987-755568
; Sequence 755568, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353.987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 755568
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-60-353-987-755568

Query Match 76.7%; Score 13.8; DB 74; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 17
|||||
Db 3 cgttacgtaagcaggg 19
|||||

RESULT 7
US-09-954-427-408320/c
; Sequence 408320, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954.427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 408320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccaromyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-09-954-427-408320

Query Match 74.4%; Score 13.4; DB 35; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 tacgtaagcctagg 18
|||||
Db 23 TACGTAAGCCTAAGA 9
|||||

RESULT 8
US-60-233-166-408320/c
; Sequence 408320, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233.166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 408320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccaromyces cerevisiae
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Affymetrix Proprieta
US-60-233-166-408320

Query Match 74.4%; Score 13.4; DB 62; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 tacgtaagcctagg 18
|||||
Db 23 TACGTAAGCCTAAGA 9
|||||

RESULT 9
US-09-956-584-493346/c
; Sequence 493346, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956.584
; CURRENT FILING DATE: 2001-09-19
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 493346
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-493346

Query Match 73.3%; Score 13.2; DB 35; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagg 18
|||||
Db 19 CGTTACTTAATCCTAAGA 2
|||||

RESULT 10
US-60-233-620-86428
; Sequence 86428, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of

; TITLE OF INVENTION: Arabidopsis thaliana
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC006136
US-60-233-620-86428

Query Match 73.3%; Score 13.2; DB 62; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 2 cgttatgtagaccttaga 19
||||| ||| |||||

RESULT 11

US-60-233-620-86434
; Sequence 86434, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Arabidopsis thaliana
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86434
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC006136
US-60-233-620-86434

Query Match 73.3%; Score 13.2; DB 62; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 5 cgttatgtagaccttaga 22
||||| ||| |||||

RESULT 12

US-60-234-017-481562/c
; Sequence 481562, Application US/602334017
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481562
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: GenBank AI662159
US-60-234-017-481562

Query Match 73.3%; Score 13.2; DB 62; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 19 CGTTACTTAATCCTAAGA 2
||||| ||| |||||

RESULT 13

US-60-353-987-21692/c
; Sequence 21692, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-21692

Query Match 73.3%; Score 13.2; DB 74; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 22 CGTATCGTAAGCCTTGA 5
||||| ||| |||||

RESULT 14

US-60-353-987-104566
; Sequence 104566, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 104566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-104566

Query Match 73.3%; Score 13.2; DB 74; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagccttaga 18
||||| ||| |||||

Db 3 cgttacgtaagccttaga 20
||||| ||| |||||

RESULT 15

US-60-353-987-586958/c
; Sequence 586958, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 586958
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-586958

Query Match 73.3%; Score 13.2; DB 74; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagcctagga 18
||| |||| ||| |||
Db 21 CGTTTCGTAACCCCTGGGA 4

Search completed: October 12, 2002, 20:42:31
Job time: 16401 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:29 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: us-09-945-131-4

Perfect score: 18

Sequence: 1 cgttacgtaagcctagga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	18	100.0	18	5	US-09-945-131-4		Sequence 4, Appli
2	13.2	73.3	25	6	US-10-215-112-1181		Sequence 1181, Ap
3	13.2	73.3	25	6	US-10-215-112-8531		Sequence 8531, Ap
4	13.2	73.3	26	5	US-09-668-890-10		Sequence 10, Appl
5	12.8	71.1	25	5	US-09-956-604-2873		Sequence 2873, Ap
6	12.8	71.1	25	6	US-10-215-112-10029		Sequence 10029, A
7	12.2	67.8	25	5	US-09-956-604-96488		Sequence 96488, A
8	12.2	67.8	25	5	US-09-956-604-96547		Sequence 96547, A
9	12.2	67.8	25	6	US-10-215-112-642		Sequence 642, App
10	12.2	67.8	25	6	US-10-215-112-3773		Sequence 3773, Ap
11	12	66.7	22	5	US-09-777-798-1		Sequence 1, Appli
12	12	66.7	25	6	US-10-215-112-3998		Sequence 3998, Ap
13	12	66.7	25	6	US-10-215-112-11520		Sequence 11520, A
14	12	66.7	25	6	US-10-215-112-12848		Sequence 12848, A
15	11.8	65.6	24	1	PCT-US02-09558-2		Sequence 2, Appli
16	11.8	65.6	25	5	US-09-956-604-96487		Sequence 96487, A
17	11.8	65.6	25	5	US-09-956-604-128739		Sequence 128739, A
18	11.8	65.6	25	5	US-09-396-196G-95431		Sequence 95431, A
19	11.8	65.6	25	5	US-09-396-196G-95432		Sequence 95432, A
20	11.6	64.4	25	5	US-09-956-604-108431		Sequence 108431, A
21	11.6	64.4	25	5	US-09-956-604-123143		Sequence 123143, A
22	11.6	64.4	25	5	US-09-396-196G-13193		Sequence 13193, A
23	11.6	64.4	25	5	US-09-396-196G-29737		Sequence 29737, A
24	11.6	64.4	25	5	US-09-396-196G-29748		Sequence 29748, A
25	11.6	64.4	25	6	US-10-215-112-1290		Sequence 1290, Ap

c 26	11.6	64.4	25	6	US-10-215-112-8657	Sequence 8657, Ap
c 27	11.4	63.3	25	5	US-09-956-604-28723	Sequence 28723, A
c 28	11.4	63.3	25	5	US-09-956-604-28724	Sequence 28724, A
c 29	11.4	63.3	25	5	US-09-956-604-28725	Sequence 28725, A
c 30	11.4	63.3	25	5	US-09-956-604-28726	Sequence 28726, A
c 31	11.4	63.3	25	5	US-09-956-604-28727	Sequence 28727, A
c 32	11.4	63.3	25	5	US-09-956-604-28728	Sequence 28728, A
c 33	11.4	63.3	25	5	US-09-956-604-28774	Sequence 28774, A
c 34	11.4	63.3	25	5	US-09-956-604-28775	Sequence 28775, A
c 35	11.4	63.3	25	5	US-09-956-604-28776	Sequence 28776, A
c 36	11.4	63.3	25	5	US-09-956-604-28777	Sequence 28777, A
c 37	11.4	63.3	25	5	US-09-956-604-28778	Sequence 28778, A
c 38	11.4	63.3	25	5	US-09-956-604-28779	Sequence 28779, A
c 39	11.4	63.3	25	5	US-09-956-604-28788	Sequence 28788, A
c 40	11.4	63.3	25	5	US-09-956-604-28807	Sequence 28807, A
c 41	11.4	63.3	25	5	US-09-396-196G-55248	Sequence 55248, A
c 42	11.4	63.3	25	5	US-09-396-196G-55249	Sequence 55249, A
c 43	11.4	63.3	30	1	PCT-US02-16308-33	Sequence 33, Appl
c 44	11.4	63.3	34	7	US-10-018-997-5	Sequence 5, Appl
c 45	11.4	63.3	34	7	US-10-018-997-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-945-131-4
; Sequence 4, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-4

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cgttacgtaagcctagga 18
| | | | | | | | | | | | | | | | | |
Db 1 cgttacgtaagcctagga 18

RESULT 2
US-10-215-112-1181
; Sequence 1181, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112

; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-1181

Query Match 73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
||| | ||||| |||||
Db 6 cgtgatgtaagcgttagga 23

RESULT 3
US-10-215-112-8531/c
; Sequence 8531, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-8531

Query Match 73.3%; Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
||| | ||||| |||||
Db 20 CGTGATGTAGCGGTAGGA 3

RESULT 4
US-09-666-890-10
; Sequence 10, Application US/09666890
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Nucleic Acid Marker Ladder For
; Estimating Mass
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/666,890

; FILING DATE: 14-Jul-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,124
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.2570000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-666-890-10

Query Match 73.3%; Score 13.2; DB 5; Length 26;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttagga 18
||| | ||||| |||||
Db 6 CGTGAGGTGAGCCGTAGGA 23

RESULT 5
US-09-956-604-2873/c
; Sequence 2873, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 2873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-2873

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cgttacgtaagccttag 16
||| | ||||| |||||
Db 23 CGITGCGGAAGCCTAG 8

RESULT 6
US-10-215-112-10029/c
; Sequence 10029, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10029


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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10029

Query Match      71.1%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctag 16
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Db 25 CGTTTCGTAAGACTAG 10

RESULT 7
US-09-956-604-96488
; Sequence 96488, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 96488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-96488

Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gttacgtaagcctagga 18
    ||| ||||| |||
Db 9 gttacgtaagctagta 25

RESULT 8
US-09-956-604-96547/c
; Sequence 96547, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 96547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-96547

Query Match      67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gttacgtaagcctagga 18
    ||| ||||| |||
Db 24 GTTAAGTAAGCTAGTA 8
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```
RESULT 9
US-10-215-112-642
; Sequence 642, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-642

Query Match      67.8%; Score 12.2; DB 6; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctag 17
    ||| ||||| |||
Db 9 cgtgatgtaagcctag 25

RESULT 10
US-10-215-112-3773/c
; Sequence 3773, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3773
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3773

Query Match      67.8%; Score 12.2; DB 6; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgttacgtaagcctag 17
    ||| ||||| |||
Db 17 CGTGATGTAAGCGTAGG 1

RESULT 11
US-09-777-798-1
; Sequence 1, Application US/09777798
; GENERAL INFORMATION:
; APPLICANT: Thompson, Steven A.
; APPLICANT: Cui, Cory
; APPLICANT: Clayton, Kathryn
; APPLICANT: Ernst, Cynthia
; TITLE OF INVENTION: HIGH OIL MAIZE PLANTS, AND METHODS FOR OBTAINING SAME
; FILE REFERENCE: DowAg/7094-143
; CURRENT APPLICATION NUMBER: US/09/777,798
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; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-777-798-1

Query Match 66.7%; Score 12; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 acgtaagcctagg 16
|||||
Db 2 acgtaagcctagg 13

RESULT 12
US-10-215-112-3998
; Sequence 3998, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3998
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3998

Query Match 66.7%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagg 17
|||||
Db 9 cgtaagcctagg 20

RESULT 13
US-10-215-112-11520
; Sequence 11520, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-11520

Query Match 66.7%; Score 12; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagg 17
|||||
Db 11 cgtaagcctagg 22

RESULT 14
US-10-215-112-12848
; Sequence 12848, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12848

Query Match 66.7%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtaagcctagg 17
|||||
Db 5 cgtaagcctagg 16

RESULT 15
PCT-US02-09558-2/c
; Sequence 2, Application PC/TUS0209558
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; TITLE OF INVENTION: Ras p27 Animal Models and Uses Thereof
; FILE REFERENCE: USF-111XC1
; CURRENT APPLICATION NUMBER: PCT/US02/09558
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/278,430
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
PCT-US02-09558-2

Query Match 65.6%; Score 11.8; DB 1; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ttacgtaagcctagg 17
|||||
Db 16 TTAAGCCTGG 2

Search completed: October 12, 2002, 17:27:30
Job time: 10805 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:17 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-6

Perfect score: 18
Sequence: 1 catgtctctcaccttga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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1	18	100.0	18	6	I33924	I33924 Sequence 2
2	13.8	76.7	33	6	A76106	A76106 Sequence 45
c 3	13.8	76.7	41	6	I68632	I68632 Sequence 5
c 4	13.2	73.3	33	6	AR014169	AR014169 Sequence
c 5	13.2	73.3	36	6	AX069513	AX069513 Sequence
c 6	13.2	73.3	36	6	AX069514	AX069514 Sequence
c 7	12.8	71.1	20	12	AB068808	AB068808 Synthetic
c 8	12.8	71.1	23	6	AX002948	AX002948 Sequence
c 9	12.8	71.1	24	6	AX002963	AX002963 Sequence
c 10	12.8	71.1	24	9	HSR270350	AJ7270350 Homo sapi
c 11	12.8	71.1	28	6	AR090768	AR090768 Sequence
c 12	12.8	71.1	28	6	AX350231	AX350231 Sequence
c 13	12.8	71.1	33	6	A84409	A84409 Sequence 24
c 14	12.8	71.1	35	23	E11199	E11199 Probe. 9/20
c 15	12.8	71.1	48	6	AX223672	AX223672 Sequence
c 16	12.8	71.1	48	6	AX274473	AX274473 Sequence
c 17	12.4	68.9	18	6	AR128932	AR128932 Sequence
c 18	12.4	68.9	23	6	AR105887	AR105887 Sequence
c 19	12.4	68.9	27	6	AR138967	AR138967 Sequence
c 20	12.4	68.9	45	6	AR083218	AR083218 Sequence
c 21	12.4	68.9	45	6	AR083219	AR083219 Sequence
c 22	12.4	68.9	50	6	I42221	I42221 Sequence 34
c 23	12.2	67.8	21	6	E07342	E07342 Primer for
c 24	12.2	67.8	23	6	AX327683	AX327683 Sequence
c 25	12.2	67.8	24	6	AX019226	AX019226 Sequence
c 26	12.2	67.8	25	6	AR165197	AR165197 Sequence
c 27	12.2	67.8	45	6	A47620	A47620 Sequence 12
c 28	12.2	67.8	45	6	A80120	A80120 Sequence 12
c 29	12.2	67.8	45	6	AX306498	AX306498 Sequence
c 30	12.2	67.8	45	6	I34331	I34331 Sequence 30
c 31	12.2	67.8	47	6	AR088055	AR088055 Sequence
c 32	12.2	67.8	47	6	AR088056	AR088056 Sequence
c 33	12.2	67.8	50	6	AX164819	AX164819 Sequence
c 34	12.2	67.8	50	9	HSR14655	AJ224655 Homo sapi
c 35	12	66.7	25	1	S58559	S58559 tRNA(GCAla
c 36	12	66.7	30	6	A62004	A62004 Sequence 34
c 37	12	66.7	30	6	AR125838	AR125838 Sequence
c 38	12	66.7	30	6	I47250	I47250 Sequence 18
c 39	12	66.7	31	6	AR112518	AR112518 Sequence
c 40	12	66.7	31	6	BD002606	BD002606 Gene comp
c 41	11.8	65.6	19	12	AB069342	AB069342 Synthetic
c 42	11.8	65.6	19	12	AB069344	AB069344 Synthetic
c 43	11.8	65.6	20	6	AR106016	AR106016 Sequence
c 44	11.8	65.6	20	6	AR153357	AR153357 Sequence
c 45	11.8	65.6	21	6	AR139560	AR139560 Sequence

ALIGNMENTS

RESULT 1	I33924	I33924	Sequence 2 from patent US 5593974.	18 bp	DNA	Linear	PAT 06-FEB-1997
I33924	LOCUS	I33924	Sequence 2 from patent US 5593974.				
	DEFINITION	I33924					
	ACCESSION	I33924					
	VERSION	I33924.1	GI:1824715				
	KEYWORDS						
	SOURCE	Unknown.					
	ORGANISM	Unknown.					
	REFERENCE	Unclassified.					
	AUTHORS	Rosenberg, R.D., Simons, M., Edelman, E., Langer, R.S. and DeKeyser, J.-L.					
	TITLE	Localized oligonucleotide therapy					
	JOURNAL	Patent: US 5593974-A 2 14-JAN-1997;					
	FEATURES	Location/Qualifiers					
	source	1. .18					
	BASE COUNT	3 a	7 c	3 g	5 t		
	ORIGIN						
	Query Match	100.0%	Score 18;	DB 6;	Length 18;		

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Best Local Similarity 100.0%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
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Db 1 CATGCTCTCCACCTTGA 18

RESULT 2
A76106
LOCUS A76106 33 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 45 from Patent WO9320210.
ACCESSION A76106
VERSION A76106.1 GI:6088247
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Taylor,G. and Stott,E.J.
TITLE ANTIBODIES FOR TREATMENT AND PREVENTION OF RESPIRATORY SYNCYTIAL
JOURNAL VIRUS INFECTION
PATENT: WO 9320210-A 45 14-OCT-1993;
SCOTGEN LTD (GB); TAYLOR GERALDINE (GB)
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 7 a 13 c 5 g 8 t
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Query Match 76.7%; Score 13.8; DB 6; Length 33;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttgg 17
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Db 16 CATGGCCACCACTTGG 32

RESULT 3
I68632/c
LOCUS I68632 41 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 5 from patent US 5677124.
ACCESSION I68632
VERSION I68632.1 GI:2830754
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS DuBois,D.B., Winkler,M.M. and Pasloske,B.L.
TITLE Ribonuclease resistant viral RNA standards
JOURNAL Patent: US 5677124-A 5 14-OCT-1997;
FEATURES
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1. .41
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BASE COUNT 15 a 7 c 10 g 9 t
ORIGIN

Query Match 76.7%; Score 13.8; DB 6; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccaccttga 18
|||||
Db 24 ATGCTCTCCAACCTAGA 8

RESULT 4
AR014169/c
LOCUS AR014169 33 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5773253.
ACCESSION AR014169
VERSION AR014169.1 GI:3971623
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Lineley,P.S., Ledbetter,J.A. and Peach,R.
TITLE MYPPIY variants of CTL A4 and uses thereof
JOURNAL Patent: US 5773253-A 12 30-JUN-1998;
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BASE COUNT 7 a 11 c 8 g 7 t
ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 33;
Best Local Similarity 83.3%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
|||||
Db 18 CATGAGCTCCACCTTGA 1

RESULT 5
AX069513
LOCUS AX069513 36 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 177 from Patent WO0102600.
ACCESSION AX069513
VERSION AX069513.1 GI:12579298
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 36)
AUTHORS Yuan,C.S.
TITLE Detection of analytes using attenuated enzymes
JOURNAL Patent: WO 0102600-A 177 11-JAN-2001;
GENERAL ATOMICS (US)
FEATURES
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1. .36
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotides for producing SAH hydrolase mutants"
BASE COUNT 8 a 15 c 7 g 6 t
ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 36;
Best Local Similarity 83.3%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
|||||
Db 18 CATCTCTCCACCCAGGA 35

RESULT 6
AX069514/c
LOCUS AX069514 36 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 178 from Patent WO0102600.
ACCESSION AX069514
VERSION AX069514.1 GI:12579299
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 36)

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AUTHORS Yuan,C.S.
 TITLE Detection of analytes using attenuated enzymes
 JOURNAL Patent: WO 0102600-A 178 11-JAN-2001;
 GENERAL ATOMICS (US)

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 Location/Qualifiers

/organism="synthetic construct"
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 /note="Oligonucleotides for producing SAH hydrolase mutants"

BASE COUNT 6 a 7 c 15 g 8 t

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 36;

Best Local Similarity 83.3%; Pred. No. 2.7e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttgga 18

Db 19 CATCTCCTCCACCCAGGA 2

RESULT 7
 AB068808/c

LOCUS AB068808 20 bp DNA linear SYN 08-AUG-2001
 DEFINITION Synthetic construct DNA, forward primer for human STS sts-IB3268 at lp36.

ACCESSION AB068808

VERSION AB068808.1 GI:15129612

KEYWORDS synthetic construct DNA.

ORGANISM synthetic construct

SOURCE synthetic construct

REFERENCE 1 (bases 1 to 20)

AUTHORS

Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
 Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
 Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
 and Soeda,E.

TITLE A bac-based sts-content map spanning a 35-mb region of human

chromosome lp35-p36

JOURNAL Genomics. 74 (1), 55-70 (2001)

MEDLINE 21269192

REFERENCE 2 (bases 1 to 20)

AUTHORS

Horii,A.

TITLE Direct Submission

JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
 Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
 Tel:81-22-717-8042, Fax:81-22-717-8047)

FEATURES Location/Qualifiers

source 1..20

/organism="synthetic construct"

/db_xref="taxon:32630"

misc_feature 1..20

/note="forward primer for human STS sts-IB3268 at lp36
 sts-IB3268 obtained from clones B13D23, B54F24, B31LL3,
 B375N12, B99F6, B99C7, Human BAC library RPCI-11"

BASE COUNT 5 a 3 c 9 g 3 t

ORIGIN

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Best Local Similarity 87.5%; Pred. No. 4.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgtctccaccttgga 18

Db 18 TGTCCCTACCTTGGGA 3

RESULT 8
 AX002948/c

LOCUS AX002948 23 bp DNA linear PAT 24-AUG-2000
 DEFINITION Sequence 1 from Patent EP0943678.
 ACCESSION AX002948
 VERSION AX002948.1 GI:9926852
 KEYWORDS synthetic construct.
 ORGANISM synthetic construct
 SOURCE artificial sequence.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Matsui,T. and Fukuyama,S.
 TITLE Lipase variants

JOURNAL Patent: EP 0943678-A 1 22-SEP-1999;
 NOVONORDISK AS (DK)
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 source 1..23
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 /db_xref="taxon:32630"
 /note="Primer 2640"

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Best Local Similarity 87.5%; Pred. No. 4.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccaccttg 17

Db 21 ATTCTCCACCTGGG 6

RESULT 9

AX002963/c

LOCUS AX002963 24 bp DNA linear PAT 24-AUG-2000

DEFINITION Sequence 16 from Patent EP0943678.

ACCESSION AX002963

VERSION AX002963.1 GI:9926867

KEYWORDS synthetic construct.

ORGANISM synthetic construct

SOURCE artificial sequence.

REFERENCE 1 (bases 1 to 24)

AUTHORS Matsui,T. and Fukuyama,S.

TITLE Lipase variants

JOURNAL Patent: EP 0943678-A 16 22-SEP-1999;
 NOVONORDISK AS (DK)

FEATURES Location/Qualifiers

source 1..24

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccaccttg 17.

Db 21 ATTCTCCACCTGGG 6

RESULT 10

HSA270350

LOCUS HSA270350 24 bp DNA linear PRI 26-JUL-2000

DEFINITION Homo sapiens EMX1 antisense primer.

ACCESSION AJ270350

VERSION AJ270350.1 GI:9557925

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS Palm,K., Salin-Nordstrom,T., Levesque,M.F. and Neuman,T.
TITLE Fetal and adult human CNS stem cells have similar molecular characteristics and developmental potential
JOURNAL Brain Res. Mol. Brain Res. 78 (1-2), 192-195 (2000)
MEDLINE 20351569
REFERENCE 2 (bases 1 to 24)
AUTHORS Palm,K.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1999) Surgery, Cedars Sinai Medical Center, 8700 Beverly Blvd., Los Angeles, CA 90048, US
COMMENT Related entry: X68879.
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
misc_feature 1..24
/note="PCR antisense primer for EMX1"
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 2 ATGCTCTCCCATTTGG 17

RESULT 11
AR090768/c
LOCUS AR090768 28 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 888 from patent US 5994076.
ACCESSION AR090768
VERSION AR090768.1 GI:10017523
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 888 30-NOV-1999;
FEATURES
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BASE COUNT 10 a 6 c 8 g 4 t
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AX350231/c
LOCUS AX350231 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 48 from Patent WO0200884.
ACCESSION AX350231
VERSION AX350231.1 GI:18615899
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequence.

1 (sites)
Galarza,J.M. and Latham,T.E.
TITLE Nucleotide sequence of influenza A/udorn/72 (h3n2) genome
JOURNAL Patent: WO 0200884-A 48 03-JAN-2002;
AMERICAN CYANAMID COMPANY (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="Primer"
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Qy 1 catgtctctccaccttg 16
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Db 25 CATGGCTCCCATG 10

RESULT 13
A84409
LOCUS A84409 33 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 24 from Patent WO9845704.
ACCESSION A84409
VERSION A84409.1 GI:6733328
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Tullin,S. and Kasper,A.
TITLE A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE
JOURNAL Patent: WO 9845704-A 24 15-OCT-1998;
TULLIN SOEREN (DK); KASPER ALMHOLT (DK)
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source Location/Qualifiers
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ORIGIN

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctctccaccttg 16
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Db 12 CATGCTGTCATCTTG 27

RESULT 14
E11199
ID E11199 standard; DNA; UNC; 35 BP.
XX XX
AC E11199;
XX XX
SV E11199.1
XX XX
DT 08-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
DE Probe.
XX JP 1996089300-A/14.
XX unidentified
OC unclassified.

XX [1]
RN 1-35
RA Tokuda C., Fukuda T., Saito I.;
RT "METHOD FOR DETECTING NUCLEIC ACID";
RL Patent number JP1996089300-A/14, 09-APR-1996.
RL MITSUI TOAISU CHEM INC, MITSUI PHARMACEUT INC.
XX

CC OS None
CC OC Artificial sequences.
CC PN JP 1996089300-A/14
CC PD 09-APR-1996
CC PF 28-SEP-1994 JP 1994232637
CC PI TOKUDA CHIKASHI, FUKUDA TAMOTSU, SAITO IZUMI
CC PC C12Q1/68,G01N33/58//C12N15/09,C12Q1/70;
CC CC strandedness: Single;
CC CC topology: Linear;
CC CC topolgy: Linear;
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SQ Sequence 35 BP; 7 A; 15 C; 6 G; 7 T; 0 other;

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Best Local Similarity 87.5%; Pred. No. 4.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacacctg 16
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Db 16 CACGTCTCCACCTCG 31

RESULT 15
AX223672/c
LOCUS AX223672 48 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 9114 from Patent WO0159103.
ACCESSION AX223672
VERSION AX223672.1 GI:15551396
KEYWORDS
SOURCE synthetic construct.
ORGANISM -synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 48)
AUTHORS Blatt,L., Mcswigen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 9114 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
Mcswigen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
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BASE COUNT 13 a 14 c 12 g 9 t
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 tgtctccacacctgga 18
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Search completed: October 12, 2002, 16:51:19
Job time: 8894 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:31 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-6
Perfect score: 18
Sequence: 1 catgctctccaccttga 18

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	14.8	82.2	30	16	US-09-228-420-5
5	14.8	82.2	30	16	US-09-228-420-9
6	14.8	82.2	30	37	US-10-006-394-5
7	14.8	82.2	30	37	US-10-006-394-9
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16	13.8	76.7	25	34	US-09-922-181A-1975
17	13.8	76.7	25	34	US-09-922-181A-1976
18	13.8	76.7	25	34	US-09-922-181A-1977
19	13.8	76.7	25	34	US-09-922-181A-1978
20	13.8	76.7	25	34	US-09-922-181A-1979
21	13.8	76.7	25	34	US-09-922-181A-1980
22	13.8	76.7	25	34	US-09-922-181A-1981
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26	13.8	76.7	25	35	US-09-956-584-309394
27	13.8	76.7	25	62	US-60-234-017-82282
28	13.8	76.7	25	62	US-60-234-017-281428
29	13.8	76.7	33	7	US-08-313-311B-45
30	13.8	76.7	41	12	US-08-841-251-5
31	13.8	76.7	41	26	US-09-665-638-5

c 32 13.4 74.4 23 1 PCT-US00-19094A-388 Sequence 388, App
c 33 13.4 74.4 23 37 US-10-010-802-388 Sequence 388, App
c 34 13.4 74.4 25 74 US-60-353-987-79860 Sequence 79860, A
c 35 13.4 74.4 25 74 US-60-353-987-280884 Sequence 280884,
c 36 13.4 74.4 48 31 US-09-827-395A-2496 Sequence 2496, Ap
c 37 13.2 73.3 20 14 US-09-071-699-20 Sequence 20, Appl
c 38 13.2 73.3 20 17 US-09-303-040-20 Sequence 20, Appl
c 39 13.2 73.3 20 17 US-09-303-510-20 Sequence 20, Appl
c 40 13.2 73.3 24 1 PCT-US00-24784-160 Sequence 160, App
c 41 13.2 73.3 24 1 PCT-US00-24784-182 Sequence 182, App
c 42 13.2 73.3 25 35 US-09-956-584-146730 Sequence 146730,
c 43 13.2 73.3 25 35 US-09-956-584-158941 Sequence 158941,
c 44 13.2 73.3 25 35 US-09-956-584-260346 Sequence 260346,
c 45 13.2 73.3 25 35 US-09-956-584-391677 Sequence 391677,

ALIGNMENTS

RESULT 1
US-09-241-561-6
; Sequence 6, Application US/09241561
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/241,561
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 60/073,554
; EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-241-561-6

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccaccttggg 18
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Db 1 catgtctccaccttggg 18

RESULT 2
US-08-465-971A-5
; Sequence 5, Application US/08465971A
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,971A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-465-971A-5

Query Match 82.2%; Score 14.8; DB 8; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttggg 18
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Db 12 CATGAATCCACCTTGGG 29

RESULT 3
US-08-465-971A-9
; Sequence 9, Application US/08465971A
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,971A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-465-971A-9

Query Match 82.2%; Score 14.8; DB 8; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
||||| ||||| |||||
Db 12 CATGAACCTCCACCTTGA 29

RESULT 4
US-09-228-420-5
; Sequence 5, Application US/09228420
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,971
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-228-420-5

Query Match 82.2%; Score 14.8; DB 16; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
||||| ||||| |||||
Db 12 CATGAACCTCCACCTTGA 29

RESULT 5
US-09-228-420-9
; Sequence 9, Application US/09228420
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/006,394
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,420
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/228,420
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,971
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-228-420-9

Query Match 82.2%; Score 14.8; DB 16; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
||||| ||||| |||||
Db 12 CATGAACCTCCACCTTGA 29

RESULT 6
US-10-006-394-5
; Sequence 5, Application US/10006394
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/006,394
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,420
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073

REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-006-394-5

Query Match 82.2%; Score 14.8; DB 37; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
||||| |||||||||
DB 12 CATGAACCTCCACCTTGA 29

RESULT 7

US-10-006-394-9
Sequence 9, Application US/10006394
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/006,394
FILING DATE: 10-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/228,420
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-006-394-9

Query Match 82.2%; Score 14.8; DB 37; Length 30;
Best Local Similarity 88.9%; Pred. No. 7e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
||||| |||||||||
DB 12 CATGAACCTCCACCTTGA 29

RESULT 8

US-08-465-971A-7
Sequence 7, Application US/08465971A
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-465-971A-7

Query Match 82.2%; Score 14.8; DB 8; Length 34;
Best Local Similarity 88.9%; Pred. No. 7.1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
||||| |||||||||
DB 16 CATGAACCTCCACCTTGA 33

RESULT 9

US-09-228-420-7
Sequence 7, Application US/09228420
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/228,420
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,971
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
US-09-228-420-7

Query Match 82.2%; Score 14.8; DB 16; Length 34;
Best Local Similarity 88.9%; Pred. No. 7.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacacttggga 18
||||| |||||||||
DB 16 CATGAACCTCCACCTTGA 33

RESULT 10
US-10-006-394-7
Sequence 7, Application US/10006394
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEP51
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/006,394
FILING DATE: 10-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/228,420
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-006-394-7

Query Match 82.2%; Score 14.8; DB 37; Length 34;
Best Local Similarity 88.9%; Pred. No. 7.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacacttggga 18
||||| |||||||||
DB 16 CATGAACCTCCACCTTGA 33

RESULT 11
US-09-338-248-101
Sequence 101, Application US/09338248
GENERAL INFORMATION:
APPLICANT: Lee, Stephen C
TITLE OF INVENTION: Method of Producing Permutins by
Scanning Permutagenesis
FILE REFERENCE: C_3041
CURRENT APPLICATION NUMBER: US/09/338,248
CURRENT FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 101
LENGTH: 36
TYPE: DNA
ORGANISM: Synthetic
US-09-338-248-101

Query Match 82.2%; Score 14.8; DB 17; Length 36;
Best Local Similarity 88.9%; Pred. No. 7.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacacttggga 18
||||| |||||||||
DB 9 catgtctccacacttggga 26

RESULT 12
US-09-956-584-422010/c
Sequence 422010, Application US/09956584
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
FILE REFERENCE: 3115.1
CURRENT APPLICATION NUMBER: US/09/956,584
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,017
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 422010
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-956-584-422010

Query Match 80.0%; Score 14.4; DB 35; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgtctccacacttggga 18
||| |||||||||
DB 17 TGTACTCCACCTTGA 2

```
RESULT 13
US-60-234-017-427909/c
; Sequence 427909, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 427909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV145609
US-60-234-017-427909

Query Match      80.0%; Score 14.4; DB 62; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgctctccaccttgg 18
   ||| ||||| |||||
Db 17 TGTACTCCACCTTGG 2

RESULT 14
US-10-017-974-25182/c
; Sequence 25182, Application US/10017974
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Lawrence
; TITLE OF INVENTION: Nucleic Acid-Based Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Nile Virus Infection
; FILE REFERENCE: MHB00,1109-A (400/037)
; CURRENT APPLICATION NUMBER: US/10/017,974
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 37080
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25182
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-017-974-25182

Query Match      80.0%; Score 14.4; DB 37; Length 48;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgctctccaccttgg 18
   | ||||| |||||
Db 16 TTCTCTCCACCTTGG 1

RESULT 15
US-09-922-181A-478/c
; Sequence 478, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
```

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; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 478
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-478

Query Match      76.7%; Score 13.8; DB 34; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctctccaccttgg 17
   || ||||| |||||
Db 17 CAGGTCTCTCCACCATGG 1

Search completed: October 12, 2002, 20:42:32
Job time: 16402 sec
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us-09-945-131-6.rnrm

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:31 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-6
Perfect score: 18
Sequence: 1 catgtctccaccttga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New: *
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq: *
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-6
2	14.4	80.0	48	7	US-10-156-306-4143
3	13.8	76.7	30	1	PCT-US02-25943-54675
4	13.8	76.7	41	7	US-10-120-013-5
5	13.4	74.4	23	7	US-10-009-678-388
6	13.2	73.3	20	1	PCT-US02-25943-28430
7	13.2	73.3	35	1	PCT-US02-25943-28431
8	13	72.2	15	1	PCT-US02-25943-62053
9	13	72.2	17	1	PCT-US02-25943-62054
10	13	72.2	19	1	PCT-US02-25943-24151
11	13	72.2	49	1	PCT-US02-25943-24149
12	12.8	71.1	24	5	US-09-992-665-105
13	12.8	71.1	25	5	US-09-396-1966-1664
14	12.8	71.1	25	5	US-09-396-1966-24560
15	12.8	71.1	25	5	US-09-396-1966-35757
16	12.8	71.1	25	5	US-09-396-1966-53939
17	12.8	71.1	28	5	US-09-225-2018-888
18	12.8	71.1	33	5	US-09-417-197-24
19	12.8	71.1	33	6	US-10-072-036-24
20	12.8	71.1	45	6	US-10-012-064-168
21	12.8	71.1	45	6	US-10-013-913A-168
22	12.8	71.1	45	6	US-10-015-385A-168
23	12.8	71.1	45	6	US-10-015-388A-168
24	12.8	71.1	45	6	US-10-015-390A-168
25	12.8	71.1	45	6	US-10-011-692A-168

26	12.8	71.1	45	6	US-10-011-795A-168	Sequence 168, App
27	12.8	71.1	45	6	US-10-012-101B-168	Sequence 168, App
28	12.8	71.1	45	6	US-10-012-753A-168	Sequence 168, App
29	12.8	71.1	45	6	US-10-015-395A-168	Sequence 168, App
30	12.8	71.1	45	6	US-10-006-746A-168	Sequence 168, App
31	12.8	71.1	45	6	US-10-011-795B-168	Sequence 168, App
32	12.8	71.1	45	6	US-10-012-064-168	Sequence 168, App
33	12.8	71.1	45	6	US-10-012-064-168	Sequence 168, App
34	12.8	71.1	45	6	US-10-020-063A-168	Sequence 168, App
35	12.8	71.1	45	7	US-10-006-063A-168	Sequence 168, App
36	12.8	71.1	45	7	US-10-006-117A-168	Sequence 168, App
37	12.8	71.1	45	7	US-10-006-130A-168	Sequence 168, App
38	12.8	71.1	45	7	US-10-006-172A-168	Sequence 168, App
39	12.8	71.1	45	7	US-10-006-768A-168	Sequence 168, App
40	12.8	71.1	45	7	US-10-017-527A-168	Sequence 168, App
41	12.8	71.1	45	7	US-10-017-610A-168	Sequence 168, App
42	12.8	71.1	45	7	US-10-006-041A-168	Sequence 168, App
43	12.8	71.1	45	7	US-10-006-818A-168	Sequence 168, App
44	12.8	71.1	45	7	US-10-012-121A-168	Sequence 168, App
45	12.8	71.1	45	7	US-10-015-386A-168	Sequence 168, App

ALIGNMENTS

RESULT 1
US-09-945-131-6
; Sequence 6, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-6

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
| | | | | | | | | | | | | | | |
Db 1 catgtctccaccttga 18

RESULT 2
US-10-156-306-4143/c
; Sequence 4143, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)

;; CURRENT APPLICATION NUMBER: US/10/156,306
;; CURRENT FILING DATE: 2002-05-28
;; NUMBER OF SEQ ID NOS: 8013
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4143
;; LENGTH: 48
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306-4143

Query Match 80.0%; Score 14.4; DB 7; Length 48;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 tgtctccacccttggg 18
Db 16 TTTCTCTCCACCTTGA 1

RESULT 3
PCT-US02-25943-54675
;; Sequence 54675, Application PC/TUS0225943
;; GENERAL INFORMATION:
;; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
;; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
;; CURRENT APPLICATION NUMBER: PCT/US02/25943
;; CURRENT FILING DATE: 2002-08-27
;; NUMBER OF SEQ ID NOS: 64158
;; SOFTWARE: Proprietary
;; SEQ ID NO 54675
;; LENGTH: 30
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
;; FEATURE:
;; LOCATION: (5356688)...(5356717)
;; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectronObjectNumber = 58582
PCT-US02-25943-54675

Query Match 76.7%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacccttgg 17
Db 6 catgtccaccaccctgg 22

RESULT 4
US-10-120-013-5/c
;; Sequence 5, Application US/10120013
;; GENERAL INFORMATION:
;; APPLICANT: Pasloske, Brittan L.
;; Brown, David
;; Dubois, Dwight
;; Winkler, Matthew
;; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
AND UTILIZATION
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/120,013
;; FILING DATE: 10-Apr-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/881,571
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/675,153
;; FILING DATE: 03-JUL-1996
;; APPLICATION NUMBER: US 60/021,145
;; FILING DATE: 03-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: AMBI:033
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 41 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-120-013-5

Query Match 76.7%; Score 13.8; DB 7; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacccttggg 18
Db 24 ATGTCTCTCCAACTTAGA 8

RESULT 5
US-10-009-678-388/c
;; Sequence 388, Application US/10009678
;; GENERAL INFORMATION:
;; APPLICANT: Genaisance Pharmaceuticals
;; APPLICANT: Denton, R. Rex
;; APPLICANT: Nandabalan, Krishnan
;; APPLICANT: Chew, Anne
;; APPLICANT: Stephens, J. Claiborne
;; APPLICANT: Duda, Amy
;; APPLICANT: Windemuth, Andreas
;; TITLE OF INVENTION: Drug Target Isoenes: Polymorphisms in the Interleukin
;; TITLE OF INVENTION: 4 Receptor Alpha Gene
;; FILE REFERENCE: MNH-0002 PCT IL4R alpha
;; CURRENT APPLICATION NUMBER: US/10/009,678
;; CURRENT FILING DATE: 2002-04-04
;; PRIOR APPLICATION NUMBER: 60/143,435
;; PRIOR FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 413
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 388
;; LENGTH: 23
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-009-678-388

Query Match 74.4%; Score 13.4; DB 7; Length 23;
Best Local Similarity 93.3%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 catgtctccaccctt 15
Db 16 CATGTCTCTACTT 2

```
RESULT 6
PCT-US02-25943-28430
; Sequence 28430, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 28430
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2751880)...(2751900)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 30446
PCT-US02-25943-28430

Query Match 73.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
   ||| ||| ||| ||| ||| |||
Db 1 catctccaccacctggga 18

RESULT 7
PCT-US02-25943-28431
; Sequence 28431, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 28431
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2751880)...(2751915)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 30447
PCT-US02-25943-28431

Query Match 73.3%; Score 13.2; DB 1; Length 35;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
   ||| ||| ||| ||| ||| |||
Db 16 catctccaccacctggga 33

RESULT 8
PCT-US02-25943-62053/c
; Sequence 62053, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 28431
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2751880)...(2751915)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 30447
PCT-US02-25943-28431

Query Match 73.3%; Score 13.2; DB 1; Length 35;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
   ||| ||| ||| ||| ||| |||
Db 16 catctccaccacctggga 33

RESULT 9
PCT-US02-25943-62054
; Sequence 62054, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62054
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6059906)...(6059922)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 66
PCT-US02-25943-62054

Query Match 72.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccacc 13
   ||| ||| ||| ||| |||
Db 15 CATGTCTCTCCACC 3

RESULT 10
PCT-US02-25943-24151
; Sequence 24151, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 24151
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2365668)...(2365686)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 25
PCT-US02-25943-24151

Query Match 72.2%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 catgtctccacc 13
    |||||
Db 1 catgtctccacc 13

RESULT 11
PCT-US02-25943-24149/c
; Sequence 24149, Application PCTUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 24149
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2365638)...(2365686)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 25934
PCT-US02-25943-24149

Query Match 72.2%; Score 13; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccacc 13
    |||||
Db 49 CAGTCTCTCCACC 37

RESULT 12
US-09-992-665-105
; Sequence 105, Application US/09992665
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-105

Query Match 71.1%; Score 12.8; DB 5; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacccttg 17
    |||||
Db 2 atgtctccacccttg 17

RESULT 13
US-09-396-196G-1664/c
; Sequence 1664, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
```

```
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1664

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacccttg 17
    |||||
Db 23 ATGTACTGCACCTTG 8

RESULT 14
US-09-396-196G-24560
; Sequence 24560, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24560

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacccttg 16
    |||||
Db 10 caggctctccagcttg 25

RESULT 15
US-09-396-196G-35757/c
; Sequence 35757, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
```

; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35757
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-35757

Query Match 71.1%; Score 12.8; DB 5; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtcctccaccttg 16
|| ||||| |||||
Db 25 CAAGTCCTGCACCTTG 10

Search completed: October 12, 2002, 17:27:31
Job time: 10806 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:31 ; Search time 1154.93 seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-7

Perfect score: 18

Sequence: 1 gatcaggcgtgcctcaaa 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New.*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	18	100.0	18	5	US-09-945-131-7		Sequence 7, Appli
2	12.8	71.1	50	6	US-10-131-831-7370		Sequence 7370, Ap
3	12.8	71.1	50	6	US-10-131-827-7370		Sequence 7370, Ap
4	12.4	68.9	25	5	US-09-396-1966-1134		Sequence 1134, Ap
5	12.4	68.9	25	5	US-09-396-1966-32558		Sequence 32558, A
6	12.4	68.9	38	7	US-10-000-467-4		Sequence 4, Appli
7	12.4	68.9	39	7	US-10-000-467-3		Sequence 3, Appli
8	12.2	67.8	21	1	PCT-US02-25943-60781		Sequence 60781, A
9	12.2	67.8	25	5	US-09-992-665-206		Sequence 206, App
10	12.2	67.8	25	5	US-09-396-1966-1135		Sequence 1135, Ap
11	12.2	67.8	25	5	US-09-396-1966-25470		Sequence 25470, A
12	12.2	67.8	25	5	US-09-396-1966-25471		Sequence 25471, A
13	12.2	67.8	25	5	US-09-396-1966-52771		Sequence 52771, A
14	12.2	67.8	25	5	US-09-396-1966-68382		Sequence 68382, A
15	12.2	67.8	29	5	US-09-426-776A-2		Sequence 2, Appli
16	12.2	67.8	35	1	PCT-US02-25943-52461		Sequence 52461, A
17	12.2	67.8	38	1	PCT-US02-25943-57045		Sequence 57045, A
18	12.2	67.8	50	5	US-09-709-201B-29		Sequence 29, Appl
19	11.8	65.6	17	7	US-10-156-306-5152		Sequence 5152, Ap
20	11.8	65.6	17	7	US-10-156-306-5992		Sequence 5992, Ap
21	11.8	65.6	25	5	US-09-956-604-55880		Sequence 55880, A
22	11.8	65.6	25	5	US-09-956-604-55913		Sequence 55913, A
23	11.8	65.6	25	5	US-09-396-1966-73		Sequence 73, Appl
24	11.8	65.6	25	5	US-09-396-1966-37713		Sequence 37713, A
25	11.8	65.6	25	5	US-09-396-1966-37714		Sequence 37714, A

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c 26 11.8 65.6 25 5 US-09-396-1966-54628 Sequence 54628, A
c 27 11.8 65.6 31 1 PCT-US02-25943-16066 Sequence 16066, A
c 28 11.8 65.6 35 5 US-09-503-138B-54 Sequence 54, Appl
c 29 11.8 65.6 35 5 US-09-503-138B-55 Sequence 55, Appl
c 30 11.8 65.6 35 7 US-10-150-407-54 Sequence 54, Appl
c 31 11.8 65.6 35 7 US-10-150-407-55 Sequence 55, Appl
c 32 11.8 65.6 45 6 US-10-012-064-345 Sequence 345, App
c 33 11.8 65.6 45 6 US-10-013-913A-345 Sequence 345, App
c 34 11.8 65.6 45 6 US-10-015-385A-345 Sequence 345, App
c 35 11.8 65.6 45 6 US-10-015-388A-345 Sequence 345, App
c 36 11.8 65.6 45 6 US-10-015-390A-345 Sequence 345, App
c 37 11.8 65.6 45 6 US-10-011-692A-345 Sequence 345, App
c 38 11.8 65.6 45 6 US-10-011-795A-345 Sequence 345, App
c 39 11.8 65.6 45 6 US-10-012-101B-345 Sequence 345, App
c 40 11.8 65.6 45 6 US-10-012-753A-345 Sequence 345, App
c 41 11.8 65.6 45 6 US-10-015-395A-345 Sequence 345, App
c 42 11.8 65.6 45 6 US-10-006-746A-345 Sequence 345, App
c 43 11.8 65.6 45 6 US-10-011-795B-345 Sequence 345, App
c 44 11.8 65.6 45 6 US-10-012-064A-345 Sequence 345, App
c 45 11.8 65.6 45 6 US-10-012-064-345 Sequence 345, App

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ALIGNMENTS

```

RESULT 1
US-09-945-131-7
; Sequence 7, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized oligonucleotide Therapy for Preventing
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-7

```

```

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 gatcaggcgtgcctcaaa 18
Db 1 gatcaggcgtgcctcaaa 18

```

```

RESULT 2
US-10-131-831-7370
; Sequence 7370, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING

```

; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131.831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7370
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-7370

Query Match 71.1%; Score 12.8; DB 6; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tcaggcgtgcctcaaa 18
| |||| |||||
Db 11 taaggcctgcctcaaa 26

RESULT 3

US-10-131-827-7370
; Sequence 7370, Application US/10131827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131.827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7370
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-7370

Query Match 71.1%; Score 12.8; DB 6; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 tcaggcgtgcctcaaa 18
| |||| |||||
Db 11 taaggcctgcctcaaa 26

RESULT 4

US-09-396-196G-1134
; Sequence 1134, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1134

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 4.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcct 14
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Db 12 gatcaggcgtgcct 25

RESULT 5

US-09-396-196G-32558/c
; Sequence 32558, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-32558

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 4.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 aggcgtgcctcaaa 18
| ||||| |||||
Db 23 AGCGGTGACTCAA 10

RESULT 6

US-10-000-467-4
; Sequence 4, Application US/10000467
; GENERAL INFORMATION:
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Tabone, John C.
; APPLICANT: Howbert, J. Jeffrey
; APPLICANT: Mulligan, John T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; FILE REFERENCE: 780068.418C3
; CURRENT APPLICATION NUMBER: US/10/000,467
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide sequence which is linked to a

; OTHER INFORMATION: nylon bead
US-10-000-467-4

Query Match 68.9%; Score 12.4; DB 7; Length 38;
Best Local Similarity 92.9%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatcaggcgctgcct 14
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Db 7 gatcaggcgcgct 20

RESULT 7

US-10-000-467-3
; Sequence 3, Application US/10000467
; GENERAL INFORMATION:
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Tabone, John C.
; APPLICANT: Howbert, J. Jeffrey
; APPLICANT: Mulligan, John T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; TITLE OF INVENTION: SENSITIVITY IN THE ANALYSIS OF BIOLOGICAL-BASED ASSAYS
; FILE REFERENCE: 780068.418C3
; CURRENT APPLICATION NUMBER: US/10/000,467
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide DMO 596
US-10-000-467-3

Query Match 68.9%; Score 12.4; DB 7; Length 39;
Best Local Similarity 92.9%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatcaggcgctgcct 14
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Db 7 gatcaggcgcgct 20

RESULT 8

PCT-US02-25943-60781/c
; Sequence 60781, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 60781
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5924871)...(5924891)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 65096
PCT-US02-25943-60781

Query Match 67.8%; Score 12.2; DB 1; Length 21;
Best Local Similarity 82.4%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gatcaggcgctgcctcaa 17
| | | | | | | | | | | | | | | |

Db 18 GGTCAGGCGCGCCTCGA 2

RESULT 9

US-09-992-665-206
; Sequence 206, Application US/09992665
; GENERAL INFORMATION:
; APPLICANT: Kala Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-206

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcaggcgctgcctcaaa 18
| | | | | | | | | | | | | | | |
Db 6 aactggcgctgcctctaa 22

RESULT 10

US-09-396-196G-1135
; Sequence 1135, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1135
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1135

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atcaggcgctgcctcaaa 18
| | | | | | | | | | | | | | | |
Db 1 atcaggagtgctctacaa 17

RESULT 11

US-09-396-196G-25470
; Sequence 25470, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack

; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25470

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atcaggcgtgcctcaaa 18
||||| |||||
Db 7 atcaggagtaccctcaca 23

RESULT 12
US-09-396-196G-25471
; Sequence 25471, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25471

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atcaggcgtgcctcaaa 18
||||| |||||
Db 1 atcaggagtaccctcaca 17

RESULT 13
US-09-396-196G-52771/C
; Sequence 52771, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52771
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52771

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaa 17
||||| |||||
Db 19 GATCAGGAGAGCATCAA 3

RESULT 14
US-09-396-196G-68382/C
; Sequence 68382, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68382
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-68382

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atcaggcgtgcctcaaa 18
||||| |||||
Db 21 ATCAGGAGTACTGAAA 5

RESULT 15
US-09-426-776A-2
; Sequence 2, Application US/09426776A
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: TAN, Nguan Soon
; APPLICANT: HO, Bow
; APPLICANT: LAM, Toong Jin
; TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ENCODING A SECRETORY SIGNAL FOR EXPRESS
; TITLE OF INVENTION: SECRETION OF HETEROLOGOUS RECOMBINANT PROTEINS
; FILE REFERENCE: 1781-0178P
; CURRENT APPLICATION NUMBER: US/09/426,776A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chloramphenicol acetyltransferase (CAT) gene forward primer de
; OTHER INFORMATION: from bacteria
US-09-426-776A-2

Query Match 67.8%; Score 12.2; DB 5; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 atcaggcgtgcctcaaa 18
||||| |||||
Db 21 ATCAGGAGTACTGAAA 5

Query Match 67.8%; Score 12.2; DB 5; Length 29;
Best Local Similarity 82.4%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 atcaggcgtgcctcaaa 18
 | | | | | | | | | |
Db 3 atcggccgtgccttaaa 19

Search completed: October 12, 2002, 17:27:32
Job time: 10807 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:16 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: us-09-945-131-5

Perfect score: 18

Sequence: 1 ggtcgggtctccggc 18

Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hlg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

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11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

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27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description

1	18	100.0	18	6	A42365	A42365 Sequence 25	
2	18	100.0	18	6	A44383	A44383 Sequence 13	
3	18	100.0	18	6	A47170	A47170 Sequence 13	
C	4	18	100.0	18	6	AR098341	AR098341 Sequence
5	18	100.0	18	6	AR098342	AR098342 Sequence	
C	6	18	100.0	18	6	AR141743	AR141743 Sequence
7	18	100.0	18	6	AR141744	AR141744 Sequence	
C	8	18	100.0	18	6	AR146396	AR146396 Sequence
9	18	100.0	18	6	AR146397	AR146397 Sequence	
10	18	100.0	18	6	AX081380	AX081380 Sequence	
11	18	100.0	18	6	AX104469	AX104469 Sequence	
12	18	100.0	18	6	AX283210	AX283210 Sequence	
13	18	100.0	18	6	AX283279	AX283279 Sequence	
14	18	100.0	18	6	AX355446	AX355446 Sequence	
15	18	100.0	18	6	BD005488	BD005488 Cationic	
16	18	100.0	18	6	I33923	I33923 Sequence 1	
17	18	100.0	18	6	I56531	I56531 Sequence 6	
C	18	100.0	18	6	I56532	I56532 Sequence 7	
19	18	100.0	18	6	I70385	I70385 Sequence 1	
20	16.4	91.1	18	6	AX104436	AX104436 Sequence	
21	16.4	91.1	18	6	AX104470	AX104470 Sequence	
22	16.4	91.1	18	6	AX355440	AX355440 Sequence	
23	16.4	91.1	18	6	AX355441	AX355441 Sequence	
24	14.8	82.2	18	6	A40324	A40324 Sequence 15	
25	14.8	82.2	18	6	A42350	A42350 Sequence 10	
26	14.8	82.2	18	6	A44382	A44382 Sequence 12	
27	14.8	82.2	18	6	A47169	A47169 Sequence 12	
28	14.8	82.2	18	6	A56644	A56644 Sequence 11	
29	14.8	82.2	18	6	A80365	A80365 Sequence 11	
30	14.8	82.2	18	6	AR091660	AR091660 Sequence	
31	14.8	82.2	18	6	AR111768	AR111768 Sequence	
32	14.8	82.2	18	6	AR123437	AR123437 Sequence	
C	33	14.8	82.2	18	6	AR144058	AR144058 Sequence
34	14.8	82.2	18	6	AR167441	AR167441 Sequence	
35	14.8	82.2	18	6	AX081343	AX081343 Sequence	
36	14.8	82.2	18	6	AX283173	AX283173 Sequence	
37	14.8	82.2	18	6	AX283239	AX283239 Sequence	
38	14.8	82.2	18	6	E05310	E05310 Anti-sense	
39	14.8	82.2	18	6	I33926	I33926 Sequence 4	
40	14.8	82.2	18	6	I84723	I84723 Sequence 11	
41	14.8	82.2	19	6	AR144059	AR144059 Sequence	
42	14.8	82.2	24	6	AR006742	AR006742 Sequence	
43	14.8	82.2	24	6	AR065943	AR065943 Sequence	
44	14.8	82.2	24	6	AR116413	AR116413 Sequence	
45	14.8	82.2	24	6	AR157686	AR157686 Sequence	

ALIGNMENTS

RESULT	1	A42365	Sequence 25 from Patent WO9501363.	18 bp	DNA	linear	PAT 05-MAR-1997
LOCUS		A42365	Sequence 25 from Patent WO9501363.				
DEFINITION		A42365					
ACCESSION		A42365.1	GI:2297841				
VERSION							
KEYWORDS							
SOURCE			unidentified.				
ORGANISM			unclassified.				
REFERENCE			1 (bases 1 to 18)				
AUTHORS			Uhlmann,E and Meier,C.				
TITLE			METHYLPHOSPHONIC ACID ESTER, PROCESS FOR PREPARING THE SAME AND ITS				
JOURNAL			US				
COMMENT			Patent: WO 9501363-A 25 12-JAN-1995;				
			HOECHST AG (DE)				
			Other publication FI 956341 960219				
			Other publication CA 2165971 950112				
			Other publication NO 955352 960214				
			Other publication AU 7073594 950124				
			Other publication DE 4321946 950112.				
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BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
|||||
Db 1 GTGTGGGGTCTCCGGGC 18

RESULT 2
A44383
LOCUS A44383 18 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 13 from Patent EP0653439.
ACCESSION A44383
VERSION A44383.1 GI:2299212
KEYWORDS house mouse.
ORGANISM Mus musculus
SOURCE house mouse.
REFERENCE 1 (bases 1 to 18)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Peyman,A.D., Uhlmann,E.D., Mag,M., Kretzchmar,G.D., Helsing,M.D.
and Winkler,I.D.
TITLE Stabilized oligonucleotids and the use thereof
JOURNAL HOECHST AG (DE)
COMMENT Other publication JP 7194385 950801
Other publication CA 2135591 950513
Other publication AU 7779994 950518
Other publication DE 438704 950518.
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exon
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
|||||
Db 1 GTGTGGGGTCTCCGGGC 18

RESULT 3
A47170
LOCUS A47170 18 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 13 from Patent EP080969.
ACCESSION A47170
VERSION A47170.1 GI:2301212
KEYWORDS house mouse.
ORGANISM Mus musculus
SOURCE Mus musculus
REFERENCE 1 (bases 1 to 18)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Seela,F.P. and Lampe,S.D.
TITLE Modified oligonucleotides, their preparation and their use
JOURNAL HOECHST AG (DE)
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COMMENT Other publication JP 8003186 960109
Other publication AU 1778295 951109
Other publication DE 4415370 951109.
FEATURES
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/organism="Mus musculus"
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/note="C-MYB"
0 a 5 c 9 g 4 t

exon
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
|||||
Db 1 GTGTGGGGTCTCCGGGC 18

RESULT 4
AR098341/C
LOCUS AR098341 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6075027.
ACCESSION AR098341
VERSION AR098341.1 GI:12807598
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Choikier,M. and Carson,D.
TITLE Treatment and prevention of hepatic disorders
JOURNAL Patent: US 6075027-A 3 13-JUN-2000;
FEATURES
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/organism="unknown"
BASE COUNT 4 a 9 c 5 g 0 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
|||||
Db 18 GTGTGGGGTCTCCGGGC 1

RESULT 5
AR098342
LOCUS AR098342 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6075027.
ACCESSION AR098342
VERSION AR098342.1 GI:12807599
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Choikier,M. and Carson,D.
TITLE Treatment and prevention of hepatic disorders
JOURNAL Patent: US 6075027-A 4 13-JUN-2000;
FEATURES
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/organism="unknown"
BASE COUNT 0 a 5 c 9 g 4 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
Db 1 GTGTCTGGGGGTCTCCGGGC 18

RESULT 6
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LOCUS      ARI14743      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6147123.
ACCESSION  ARI14743
VERSION     ARI14743.1 GI:15101259
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Chojkier,M. and Carson,D.
TITLE       Treatment and prevention of hepatic disorders
JOURNAL     Patent: US 6147123-A 3 14-NOV-2000;
FEATURES    Location/Qualifiers
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Db 18 GTGTCTGGGGGTCTCCGGGC 1

RESULT 9
ARI146397
LOCUS      ARI146397      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6218437.
ACCESSION  ARI146397
VERSION     ARI146397.1 GI:15109586
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Chojkier,M.
TITLE       Treatment and prevention of hepatic disorders
JOURNAL     Patent: US 6218437-A 4 17-APR-2001;
FEATURES    Location/Qualifiers
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BASE COUNT  0 a 5 c 9 g 4 t
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Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
Db 1 GTGTCTGGGGGTCTCCGGGC 18

RESULT 10
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LOCUS      AX081380      18 bp      DNA      linear      PAT 27-FEB-2001
DEFINITION Sequence 59 from Patent WO0108707.
ACCESSION  AX081380
VERSION     AX081380.1 GI:13170222
KEYWORDS    .
SOURCE      synthetic construct.
ORGANISM    synthetic construct
             artificial sequence.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE       Conjugates and methods for the production thereof, and their use
             for transporting molecules via biological membranes
JOURNAL     Patent: WO 0108707-A 59 08-FEB-2001;
FEATURES    Location/Qualifiers
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             /organism="unknown"
BASE COUNT  0 a 5 c 9 g 4 t
ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
Db 1 GTGTCTGGGGGTCTCCGGGC 18

RESULT 7
ARI14744
LOCUS      ARI14744      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6147123.
ACCESSION  ARI14744
VERSION     ARI14744.1 GI:15101260
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Chojkier,M. and Carson,D.
TITLE       Treatment and prevention of hepatic disorders
JOURNAL     Patent: US 6147123-A 4 14-NOV-2000;
FEATURES    Location/Qualifiers
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             1..18
             /organism="unknown"
BASE COUNT  0 a 5 c 9 g 4 t
ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 GTGTCTGGGGGTCTCCGGGC 1

RESULT 8
ARI146396/c
LOCUS      ARI146396      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6218437.
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/Note=" Oligonucleotide"
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BASE COUNT
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTCGGGTCTCCGGC 18

RESULT 11
AX104469
LOCUS AX104469 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 661 from Patent WO0122972.
ACCESSION AX104469
VERSION AX104469.1 GI:13920666
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieger,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 661 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
1..18
/organism="synthetic construct"
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0 a 5 c 9 g 4 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 GTGTCGGGTCTCCGGC 18

RESULT 12
AX283210
LOCUS AX283210 18 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 48 from Patent WO0179216.
ACCESSION AX283210
VERSION AX283210.1 GI:17044091
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing them
JOURNAL Patent: WO 0179216-A 48 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/Note="Beschreibung der kuenstlichen
Sequenz:Oligonukleotide"
0 a 5 c 9 g 4 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggtctccggc 18
|||||
Db 1 GTGTCGGGTCTCCGGC 18

RESULT 13
AX283279
LOCUS AX283279 18 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 43 from Patent WO0179249.
ACCESSION AX283279
VERSION AX283279.1 GI:17044160
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing the same
JOURNAL Patent: WO 0179249-A 43 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source
1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
/Note="Beschreibung der kuenstlichen Sequenz:
Oligonukleotide"
0 a 5 c 9 g 4 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggtctccggc 18
|||||
Db 1 GTGTCGGGTCTCCGGC 18

RESULT 14
AX355446
LOCUS AX355446 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 474 from Patent WO0197843.
ACCESSION AX355446
VERSION AX355446.1 GI:18620114
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 474 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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/db_xref="taxon:32630"
/Note="Synthetic oligonucleotide-phosphodiester backbone"
0 a 5 c 9 g 4 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 1 GTGTGGGGTCTCCGGC 18

RESULT 15
BD005488 18 bp DNA linear PAT 31-JAN-2002
LOCUS Cationic polymer and lipoprotein-containing system for gene
DEFINITION delivery.
ACCESSION BD005488
VERSION BD005488.1 GI:18633859
KEYWORDS JP 2001501812-A/1.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Maruyama,A., Akaike,T. and Kim,S.W.
TITLE Cationic polymer and lipoprotein-containing system for gene
delivery
JOURNAL Patent: JP 2001501812-A 1 13-FEB-2001;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2001501812-A/1
PD 13-FEB-2001
PF 03-JUL-1997 JP 1998504522
PR
PI JIN SEOK KIM,ATSUSHI MARUYAMA,TOSHIHIRO AKAIKE,SUNG WAN KIM PC
C12N15/64

CC Location/Qualifiers
FH Key 1..18
FT source /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 0 a 5 c 9 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gtgtcgggggtctccgggc 18
|||||
Db 1 GTGTGGGGTCTCCGGC 18

Search completed: October 12, 2002, 16:51:17
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:03 ; Search time 792.17 Seconds
(without alignments)
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Title: US-09-945-131-5

Perfect score: 18

Sequence: 1 ggtcgggtctccggc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAQ42217	Antisense sequence
2	18	100.0	18	AAQ34766	Murine c-myb antis
3	18	100.0	18	AAQ37635	Antisense oligonuc
4	18	100.0	18	AAQ44437	Antisense oligonuc
5	18	100.0	18	AAQ88725	Mouse c-myc modifi
6	18	100.0	18	AAQ28320	Multi-G oligonucle
7	18	100.0	18	AAQ17811	Glycosaminoglycan
8	18	100.0	18	AAQ17812	Glycosaminoglycan
9	18	100.0	18	AAQ93470	C-myb antisense ol

10	18	100.0	18	AAQ13831	C-myb phosphorothi
11	18	100.0	18	AAF99482	Immunostimulatory
12	18	100.0	18	AAF60950	Anti-c-myb oligonu
13	18	100.0	18	AAF86998	Rat c-myb phosphor
14	18	100.0	18	AAF86999	Rat c-myb phosphor
15	18	100.0	18	AAH49233	Anti-c-myb oligonu
16	18	100.0	18	ABL01642	Multi-G oligonucle
17	16.4	91.1	18	AAT28319	Multi-G oligonucle
18	16.4	91.1	18	AAT28323	Multi-G oligonucle
19	16.4	91.1	18	AAT28317	Immunostimulatory
20	16.4	91.1	18	AAF99473	Immunostimulatory
21	16.4	91.1	18	AAF99483	Immunostimulatory
22	16	88.9	17	AAQ87994	Antisense oligonuc
23	14.8	82.2	18	AAQ25506	Antisense nucleic
24	14.8	82.2	18	AAQ31577	c-myb mRNA complem
25	14.8	82.2	18	AAQ31560	c-myb mRNA complem
26	14.8	82.2	18	AAQ42220	Antisense sequence
27	14.8	82.2	18	AAQ35159	Human c-myb antis
28	14.8	82.2	18	AAQ41938	Human c-myb gene m
29	14.8	82.2	18	AAQ64704	c-myb antisense ol
30	14.8	82.2	18	AAQ64705	c-myb sense oligon
31	14.8	82.2	18	AAQ44436	Antisense oligonuc
32	14.8	82.2	18	AAQ92406	C-myb antisense ol
33	14.8	82.2	18	AAQ88724	Human c-myc modifi
34	14.8	82.2	18	AAQ24194	Phosphononoester
35	14.8	82.2	18	AAQ33910	c-myb expression i
36	14.8	82.2	18	AAQ44240	c-myb antisense co
37	14.8	82.2	18	AAQ28325	Multi-G oligonucle
38	14.8	82.2	18	AAQ17813	Glycosaminoglycan
39	14.8	82.2	18	AAQ93120	c-myb sense OPT.
40	14.8	82.2	18	AAQ65963	Antisense oligonuc
41	14.8	82.2	18	AAQ28155	Antisense oligonuc
42	14.8	82.2	18	AAQ23585	Deletion sequence
43	14.8	82.2	18	AAQ18676	Target c-myb antis
44	14.8	82.2	18	AAQ99427	Antisense oligonuc
45	14.8	82.2	18	AAQ98653	Human c-myb therap

ALIGNMENTS

RESULT 1	
AAQ42217	
ID	AAQ42217 standard; DNA; 18 BP.
XX	
AC	AAQ42217;
XX	
DT	02-SEP-1993 (first entry)
XX	
DE	Antisense sequence to mouse c-myb.
XX	
KW	Antisense; oligonucleotide; inhibit; translation; transcription;
KW	target; nucleic acid; mammal; tissue; hybridise; combine; carrier;
KW	polyethylene oxide; polypropylene oxide; copolymer; ss.
XX	
OS	Synthetic.
XX	
PN	WO9308845-A.
XX	
PD	13-MAY-1993.
XX	
PF	05-NOV-1992; 92WO-US09626.
XX	
PR	08-NOV-1991; 91US-0792146.
XX	
PR	18-MAR-1992; 92US-0855416.
XX	
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.
XX	
PI	Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
PI	Simons M;
XX	
DR	WPI; 1993-167406/20.
XX	

PT Inhibiting translation or transcription of target nucleic acid -
PT by local administration in vivo of oligo:nucleotide complementary
PT to target sequence
XX
XX Disclosure: Page 39; 65pp; English.
XX
CC The sequences given in AAQ42217-21 are antisense oligonucleotides
CC which were used to inhibit translation or transcription of target
CC nucleic acids at a locus in vivo. The oligonucleotide are applied
CC directly to a tissue at the locus within the body of a mammal and
CC they are able to penetrate the cells of the tissue, hybridise/combine
CC with the target nucleic acid inhibiting intracellular translation or
CC transcription. The oligonucleotide are incorporated into a carrier
CC eg. a polyethylene oxide-polypropylene oxide copolymer.
XX
XX Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtgtcgggggtctccgggc 18
|||||
DB 1 gtgtcgggggtctccgggc 18

RESULT 2
AAQ34766
ID AAQ34766 standard; DNA; 18 BP.
XX
AC AAQ34766;
XX
DT 02-JUN-1993 (first entry)
XX
DE Murine c-myb antisense oligonucleotide.
XX
KW Antisense; inhibit; protein coding genes; regulatory DNA; stroke;
KW endonuclease; vascular restenosis; myocardial infarction; embolism;
KW peripheral muscular disease; peripheral angioplasty; thrombophlebitis;
KW vasculitis; angina; Budd-Chiari syndrome; thrombosis; atherosclerosis;
KW hypertension; primary pulmonary; proliferative glomerulonephritis;
KW acute respiratory distress syndrome; idiopathic pulmonary fibrosis;
KW emphysema; ss.
XX
OS Synthetic.
XX
PN WO9301286-A.
XX
PD 21-JAN-1993.
XX
PF 23-JUN-1992; 92WO-US05305.
XX
PR 28-JUN-1991; 91US-0723454.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI DeKeyser J, Edelman E, Langer RS, Rosenberg RD;
PI Simons M;
XX
XX WPI; 1993-045491/05.
XX
XX Localised therapy using anti-sense oligo:nucleotide(s) - which
PT penetrate through tissue cell to hybridise with target m-RNA and
PT inhibit expression of the gene, for treatment of vascular
PT disorders, atherosclerosis, hypertension, etc.
XX
XX Disclosure: Page 21; 59pp; English.
PS
XX The sequences given in AAQ34766-67 and AAQ35258-60 are antisense
CC oligonucleotides which were used in a method of inhibiting a target
CC nucleic acid sequence. The method may be used for inhibiting the
CC expression of protein coding genes as well as regulatory DNA.
XX

CC Application of the antisense oligonucleotides to a defined locus in
CC vivo allows their use when systemic administration is not possible,
CC ie. systemically administered oligos may be rendered inefficient by
CC endonucleases before they reach their targets. This method may be
CC used in the treatment of vascular disorders, particularly vascular
CC restenosis, myocardial infarction, peripheral muscular disease;
CC peripheral angioplasty, thrombophlebitis, stroke, embolism,
CC vasculitis, angina, Budd-Chiari syndrome, thrombosis, atherosclerosis,
CC hypertension, primary pulmonary hypertension, proliferative glomerulo-
CC nephritis, acute respiratory distress syndrome, idiopathic pulmonary
CC fibrosis or emphysema.
XX
XX Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtgtcgggggtctccgggc 18
|||||
DB 1 gtgtcgggggtctccgggc 18

RESULT 3
AAQ37635
ID AAQ37635 standard; DNA; 18 BP.
XX
AC AAQ37635;
XX
DT 18-JUN-1993 (first entry)
XX
DE Antisense oligonucleotide to mouse c-myb codons 2-7.
XX
KW Erythrocyte; red blood cell; precursor; haemoglobin; Hb; anaemia;
KW oncogene; haematopoiesis; P75 c-myb; ss.
XX
OS Synthetic.
XX
PN WO9302654-A.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-US06685.
XX
PR 09-AUG-1991; 91US-0742867.
XX
PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Sytkowski AJ;
XX
XX WPI; 1993-076139/09.
XX
XX Haemoglobin synthesis inducement in red blood precursor cells -
PT by decreasing levels of differentiation regulator proteins e.g.
PT P75 c-myb regulating transcription of cellular genes for high
PT haemoglobin content
XX
XX Example 4; Page 26; 32pp; English.
XX
XX The product of c-myb is the differentiation regulator protein P75c-
CC myb. Downregulation of this gene, e.g. by antisense oligonucleotides,
CC results in an increase in haemoglobin production in red blood cell
CC precursors. The precursor cells can then be used in the treatment of
CC anaemia or other disorders which result from decreased oxygen-
CC carrying capacity. Oligonucleotide AAQ37635 is an example of an
CC antisense oligonucleotide for inducing Hb synthesis; 17% of cells
CC treated with AAQ37635 were haemoglobinised (Hb+) after 48 hours.
CC Treatment of replicate cultures with antisense c-myb and EPO
CC simultaneously yielded 18% Hb+ cells. The absence of an additive
CC effect suggests that both agents are operating on the same
CC responsive population of cells.
XX

SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18
 |||||
 Db 1 gtgtcgggggtctccgggc 18

RESULT 4
 AAT44437
 ID AAT44437 standard; DNA; 18 BP.
 XX
 AC AAT44437;
 XX
 DT 27-JAN-1997 (first entry)
 XX
 DE Antisense oligonucleotide against c-myb.
 XX
 KW 8-azapurine; modification; stronger complex; inhibition; ss.
 XX
 OS Synthetic.
 XX
 PN EP680969-A2.
 XX
 PD 08-NOV-1995.
 XX
 PF 26-APR-1995; 95EP-0106230.
 XX
 PR 02-MAY-1994; 94DE-4415370.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Lampe S, Seela F;
 XX
 PI WPI; 1995-375165/49.
 XX
 DR New oligo:nucleotide(s) contg. 8-aza:purine base - useful as
 PT therapeutic and diagnostic agents with more stable hybridisation to
 PT target nucleic acid
 XX
 PS Disclosure; Page 39; 51pp; German.
 XX
 CC AAT44425-54 are antisense oligonucleotides which have at least one
 CC 8-azapurine base. The presence of an 8-azapurine base results in
 CC significantly stronger complexing when hybridising to target nucleic
 CC acids. The present sequence is against c-myb.
 XX
 SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18
 |||||
 Db 1 gtgtcgggggtctccgggc 18

RESULT 5
 AAQ88725
 ID AAQ88725 standard; DNA; 18 BP.
 XX
 AC AAQ88725;
 XX
 DT 27-FEB-1996 (first entry)
 XX
 DE Mouse c-myc modified antisense oligonucleotide.
 XX

antisense; analogue; non-terminal pyrimidine; phosphorothioate;
 backbone; treatment; HIV; human immunodeficiency virus; HSV;
 herpes simplex virus; cancer; integrin; cell adhesion receptor;
 infection; diagnosis; nuclease resistance; ss.
 XX
 OS Mus musculus.
 XX
 PN EP653439-A2.
 XX
 PD 17-MAY-1995.
 XX
 PF 07-NOV-1994; 94EP-0117513.
 XX
 PR 12-NOV-1993; 93DE-4338704.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Heisberg M, Kretzschmar G, Mag M, Peyman A, Uhlmann E;
 PI Winkler I;
 XX
 DR WPI; 1995-180677/24.
 XX
 PT New anti-sense oligo:nucleotide analogues - with modified
 PT non-terminal pyrimidine nucleotide units, useful for treating viral
 PT infections, cancer, etc.
 XX
 PS Disclosure; Page 25; 36pp; German.
 XX
 CC The antisense oligonucleotide (ON) shown is a derivative of an
 CC equivalent wild type mouse c-myc ON, in which at least one, esp. 2-10,
 CC non-terminal pyrimidine nucleotide(s) is/are modified. The modification
 CC may be: (a) replacement of a phosphodiester linkage by: a
 CC phospho-thioate (PS), -dithioate, -aramidate; borano-, alkyl-,
 CC aralkyl-phosphate; 2,2,2-trichloro-1,1dimethyl-, alkyl- or aryl-,
 CC phosphonate linkage; or (3'-thio)formacetal, methylhydroxylamine, oxime,
 CC methylenedimethylhydrazo, dimethylene sulphone or silyl linkage; (b)
 CC replacement of a sugar phosphate backbone by a 'morpholinonucleoside'
 CC oligomer; (c) replacement of beta-D-2-deoxyribose by another sugar or
 CC carbocyclic, open-chain or bicyclic sugar analogue; or (c) replacement
 CC of the natural nucleoside base by an analogue, e.g.
 CC 5-hydroxymethyl-uridine. The 5' and/or 3' terminus may also be modified
 CC with a lipophilic gp., eg. a farnesyl. The modifications increase
 CC nuclease resistance and thus improve stability and activity.
 XX
 SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18
 |||||
 Db 1 gtgtcgggggtctccgggc 18

RESULT 6
 AAT28320
 ID AAT28320 standard; DNA; 18 BP.
 XX
 AC AAT28320;
 XX
 DT 19-NOV-1996 (first entry)
 XX
 DE Multi-G oligonucleotide mu AS (G4).
 XX
 KW Multi-G oligonucleotide; antisense sequence; c-myb; nuclease resistant;
 KW phosphorothioate linkage; phosphorothioate linkage; inhibitor; therapy;
 KW cell proliferation; smooth muscle cell; proliferation protein;
 KW vascular restenosis; arterial restenosis; ss.
 XX
 OS Synthetic.
 XX

FT /*tag= a
FT /note= "phosphorothioate backbone"

PN WO9608559-A1.

XX 21-MAR-1996.

XX 13-SEP-1995; 95WO-AU00600.

XX 14-AUG-1995; 95AU-0004769.

PR 16-SEP-1994; 94AU-0008226.

PR 16-SEP-1994; 94AU-0008227.

XX (CARD-) CARDIAC CRC NOMINEES PTY LTD.

PA Graham L, Underwood PA;

PI WPI; 1996-179936/18.

XX Oligo:nucleotide(s) having sulphur substns. between nucleoside(s) -
PT for inhibiting glycosaminoglycan-degrading enzymes, for treating,
PT e.g. cancer, inflammation, infection or autoimmune disorders.

XX Example 2; Page 33; 73pp; English.

XX AAT17805-T17808, and AAT17810-T17813 represent
CC glycosaminoglycan-degrading enzyme (GDE) inhibitors. The GDEs which
CC these sequences inhibit are endoglycosidases (which cleave
CC glycosaminoglycan chains at internal sites), preferably heparanases (also
CC known as heparitinases) of mammalian or bacterial origin. These
CC sequences can be used for inhibiting GDEs associated with platelets,
CC macrophages, neutrophils, leukocytes, endothelial cells, smooth muscle
CC cells, carcinoma and tumour cells, and bacteria. They can also be used
CC to inhibit smooth muscle cell activation, proliferation or migration.
CC The sequences can be used to treat cancer, inflammation, autoimmune
CC disorders, infection caused by pathogenic organisms, and cardiovascular
CC disease, such as vascular hyperplasia, restenosis and atherosclerosis.
CC These inhibitors can also be used as biochemical reagents for studying
CC GDE activities and mechanisms of enzyme activity.

XX Sequence 18 BP; 4 A; 9 C; 5 G; 0 U; 0 other;

Query Match 100.0%; Score 18; DB 17; Length 18;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18

Db 18 GTGTGGGGTCTCCGGGC 1

RESULT 9

AAT93470

ID AAT93470 standard; DNA; 18 BP.

XX AAT93470;

AC AAT93470;

XX 16-FEB-1998 (first entry)

XX C-myb antisense oligonucleotide.

XX c-myb antisense oligonucleotide; biocompatible polymer; plasmid DNA;
KW cell transformation; gene therapy; high density lipoprotein; HDL;
KW low density lipoprotein; LDL; ss.

XX Synthetic.

XX US5679559-A.

PN 21-OCT-1997.

XX 03-JUL-1996; 96US-0675120.

XX 03-JUL-1996; 96US-0675120.
PR (UTAH) UNIV UTAH RES FOUND.
PA Akaike T, Kim J, Kim SW, Maruyama A;
PI WPI; 1997-525726/48.
XX Composition for delivering nucleic acid to a cell - comprising
XX complex of nucleic acid with hydrophobised cationic biocompatible
XX polymer and lipoprotein
XX Claim 10; Column 9; 10pp; English.
XX This c-myb antisense oligonucleotide is used in the preparation of a
XX gene delivery composition. The composition comprises a complex of the
XX nucleic acid to be delivered to a cell with a hydrophobised cationic
XX biocompatible polymer and a lipoprotein. One part of the polymer and
XX one part of the lipoprotein can be combined with either one part plasmid
XX DNA or 0.001 to 0.05 parts of this oligonucleotide. The composition is
XX used for transforming cells in vitro.
XX Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 18;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18

Db 1 gtgtcgggggtctccgggc 18

RESULT 10

AAAL3831

ID AAAL3831 standard; DNA; 18 BP.

XX AAAL3831;

XX 27-JUL-2000 (first entry)

XX C-myb phosphorothioate antisense oligonucleotide SEQ ID NO:5.

XX Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW recurrent stenosis; cardiovascular injury; ss.

XX Mus sp.

XX Key Location/Qualifiers

FH modified_base 1..18

FT /*tag= a

FT /note= "phosphorothioate linkages"

XX CA2228977-A1.

XX 07-MAY-1999.

XX 03-FEB-1998; 98CA-2228977.

XX 07-NOV-1997; 97CA-2215360.

XX (EDEL/) EDELMAN E R.

XX (ROSE/) ROSENBERG R D.

XX (SIRO/) SIROIS M G.

XX (SINO/) SIMONS M.

XX Edelman ER, Rosenberg RD, Sirolis MG, Simons M;

PI WPI; 2000-283933/25.

XX

PT Antisense inhibition of platelet derived growth factor beta-receptor
PT subunit expression for the prevention of restenosis -
PS Claim 27; Page 23; 43pp; English.
XX
CC A method has been developed for preventing restenosis following vascular
CC injury by antisense inhibition of platelet derived growth factor
CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
CC canal), especially of a valve in the heart, after surgical correction of
CC the primary condition) following cardiovascular injury. The present
CC sequence represents a phosphorothioate antisense oligonucleotide for
CC c-myb.
XX
SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccggc 18
Db 1 gtgtcggggtctccggc 18

RESULT 11
AAF99482
ID AAF99482 standard; DNA; 18 BP.
XX
AC AAF99482;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #598.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US26383.
XX
PR 25-SEP-1999; 99US-0156113.
PR 27-SEP-1999; 99US-0156135.
PR 23-AUG-2000; 2000US-0227436.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
XX
PS Claim 101; Page 51; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccggc 18
Db 1 gtgtcggggtctccggc 18

RESULT 12
AAF60950
ID AAF60950 standard; DNA; 18 BP.
XX
AC AAF60950;
XX
DT 15-MAY-2001 (first entry)
XX
DE Anti-c-myb oligonucleotide SEQ ID 59.
XX
KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;
KW tumor therapy; drug; ss.
XX
OS Unidentified.
XX
PN DE19935302-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-1999; 99DE-1035302.
XX
PR 28-JUL-1999; 99DE-1035302.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX
DR WPI; 2001-203679/21.
XX
PT New substituted aryl conjugates of parent molecules, especially
PT oligonucleotides, having improved transmembrane and intracellular
PT transport properties, useful as medicaments or diagnostic agents -
XX
PS Disclosure; Page 8; 28pp; German.
XX
CC This invention describes a novel conjugate (I) which consists of (A) a
CC molecule to be transported and (B) at least one aryl residue of formula
CC -Ar-(X-C(Y)-R₁)-n (II). Ar = group containing at least one aromatic
CC ring; X = O or N (sic); Y = O, S or NH-R₂ (sic); R₁ = optionally
CC substituted 1-23C alkyl (optionally containing double and/or triple
CC bonds); R₂ = optionally substituted 1-18C alkyl (optionally containing
CC double and/or triple bonds); n = integer of 1 or more. (A) is bonded to
CC (B) directly or via a chemical group, provided that the chemical group is
CC other than CH₂-S if the bond is via a phosphodiester linkage of (A). The
CC invention also describes (i) the preparation of a conjugate (I') of (A')
CC a molecule to be transported and (B') at least one aryl residue (not
CC restricted to (II)), by preparing (A') containing a reactive function at
CC the position at which (B') is to be bonded, preparing (B') and reacting
CC (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded
CC via a chemical group) for transporting (A) across biological membranes.
CC The products of the invention have cytostatic, virucide, vasotropic,
CC dermatological, antipsoriatic and antiasthmatic activity and can be used
CC for gene therapy. Conjugation of (A) with (B) is useful for transporting

CC (A) across biological membranes or into eukaryotic or prokaryotic cells
CC (specifically bacterial, yeast or mammalian cells, including human cells,
CC particularly tumor cells). Medicaments, diagnostic agents and test kits
CC containing (I) are also claimed. Typically (I) are antisense
CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
CC treating viral infections or diseases associated with integrins or
CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);
CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
CC hybridization. Conjugation with (B) markedly improves the cellular uptake
CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
CC in which case the conjugates (I) are fluorescently labeled, allowing
CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
CC is superior to that obtained using other conjugated groups related to
CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
CC the scope of (B)) have superior uptake to corresponding fluorescein
CC conjugates.

XX SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtgtcgggggtctccgggc 18
|||||
Db 1 gtgtcgggggtctccgggc 18

RESULT 13
AAF86998/c

ID AAF86998 standard; DNA; 18 BP.

XX AC AAF86998;

XX DT 13-JUL-2001 (first entry)

XX DE Rat c-myb phosphorothioate sense oligonucleotide.

XX KW Rat; NfkappaB; vitamin E; hepatitis C virus; chronic liver disease;
XX KW hepatic fibrosis; phosphorothioate backbone; 2,6-di-tert-butylphenol; ss.
XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT modified_base 1..18

XX FT /*tag= a

XX FT /mod_base= "OTHER"

XX FT /note= "phosphorothioate backbone"

XX PN WO200121166-A1.

XX PD 29-MAR-2001.

XX PF 21-SEP-2000; 2000WO-US25956.

XX PR 21-SEP-1999; 99US-0400322.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chojkier M;

XX DR WPI; 2001-354755/37.

XX PT Treatment of patients suffering from hepatitis C comprises
XX PT administration of a 2,6-di-tert-butylphenol derivative -

XX PS Example 2; Page 39; 81pp; English.

XX CC The present invention describes a method of treating hepatitis C virus
XX CC infection, involving administering a 2,6-di-tert-butylphenol derivative
XX CC to the affected individual. This is particularly useful in patients
XX CC refractory to interferon. The present sequence is a sense oligonucleotide

CC with a phosphorothioate backbone, directed at the rat c-myb sequence in a
CC stellate cell inhibition assay described in the exemplification of the
CC invention.

XX SQ Sequence 18 BP; 4 A; 9 C; 5 G; 0 U; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtgtcgggggtctccgggc 18

|||||

Db 18 GTGTGGGGGTCTCCGGGC 1

RESULT 14

AAF86999

ID AAF86999 standard; DNA; 18 BP.

XX AC AAF86999;

XX DT 13-JUL-2001 (first entry)

XX DE Rat c-myb phosphorothioate antisense oligonucleotide.

XX KW Rat; NfkappaB; vitamin E; hepatitis C virus; chronic liver disease;
XX KW hepatic fibrosis; phosphorothioate backbone; 2,6-di-tert-butylphenol; ss.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

XX FT modified_base 1..18

XX FT /*tag= a

XX FT /mod_base= "OTHER"

XX FT /note= "phosphorothioate backbone"

XX PN WO200121166-A1.

XX PD 29-MAR-2001.

XX PF 21-SEP-2000; 2000WO-US25956.

XX PR 21-SEP-1999; 99US-0400322.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chojkier M;

XX DR WPI; 2001-354755/37.

XX PT Treatment of patients suffering from hepatitis C comprises
XX PT administration of a 2,6-di-tert-butylphenol derivative -

XX PS Example 2; Page 39; 81pp; English.

XX CC The present invention describes a method of treating hepatitis C virus
XX CC infection, involving administering a 2,6-di-tert-butylphenol derivative
XX CC to the affected individual. This is particularly useful in patients
XX CC refractory to interferon. The present sequence is an antisense
XX CC oligonucleotide with a phosphorothioate backbone, directed at the rat
XX CC c-myb sequence in a stellate cell inhibition assay described in the
XX CC exemplification of the invention.

XX SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtgtcgggggtctccgggc 18

|||||

Db 1 gtgtcggggtctccgggc 18

RESULT 15

AAH49233
ID AAH49233 standard; DNA; 18 BP.

XX AC AAH49233;

DT 26-NOV-2001 (first entry)

XX DE Anti-c-myb oligonucleotide XXVI.

XX Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.

XX OS Synthetic.

XX PN EP1113021-A2.

XX PD 04-JUL-2001.

XX PF 08-MAR-1995; 2001EP-0104012.

XX PR 14-MAR-1994; 94DE-4408528.

XX PR 08-MAR-1995; 95EP-0103332.

XX PA (AVET) AVENTIS PHARMA DEUT GMBH.

XX PI Uhlmann E, Breipohl G;

XX WPI; 2001-591267/67.

XX PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
for treating e.g. cancer, also as diagnostic probes and primers

XX PS Disclosure; Page 25; 54pp; German.

XX This invention describes novel polyamide-oligonucleotide derivatives (I)
and their physiologically acceptable salts of formula
CC F((DNA)-Li)-q(PNA)-Li)-r(DNA)-Li)-s(PNA)-t)-xf' where q, r, s, t = 0 or 1,
CC with the sum of two or more adjacent letters at least 2; x = 1-20; DNA
CC = nucleic acid (such as DNA or RNA or their known derivatives); Li =
CC covalent linkage between DNA and PNA, i.e. a bond or a residue containing
CC at least one atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide
CC structure containing at least one nucleobase different from thymine; and
CC F, F' = end groups and/or are connected through a covalent bond. The
CC products of the invention have anticancer, antiproliferative, antiviral,
CC hepatotropic and vasotropic activity and can be used for the inhibition
CC of gene expression by antisense, ribozyme, sense, or triple-helix
CC methods, or by binding to proteins (aptamers). (I) are used for treating
CC diseases caused by viruses (human immune deficiency, herpes simplex,
CC influenza, vesicular stomatitis, hepatitis B or papilloma), or mediated
CC by integrins or cell-cell adhesion reactions, for treating cancer, or
CC for inhibiting restenosis, particularly as antisense reagents. They are
CC also useful in heterogeneous or homogeneous assays as primers or probes,
CC particularly where the target is amplified before being detected by
CC hybridization, for diagnosis of genetic, malignant or pathogen-related
CC diseases. (I) retain the increased affinity for complementary strands and
CC better stability in serum, associated with conventional peptide nucleic
CC acids (PNA), but lack the disadvantages, i.e. have improved cellular
CC uptake, do not aggregate in aqueous solution, and have reduced affinity
CC for purification materials, reduced cytotoxicity, better sequence
CC specificity. They are more active than either DNA or PNA oligomers. When
CC used as probes, (I) show different responses to base-pair mismatches in
CC the DNA and PNA segments, allowing better discrimination between
CC pathogenic and non-pathogenic conditions such as the transition from
CC proto-oncogene to oncogene, also, when used as primers, with the PNA
CC segment at the 5'-end, they produce amplicons resistant to
CC 5'-exonuclease, allowing this enzyme to be used to eliminate RNA or DNA
CC primers. The DNA component allows additional reactions not possible with

CC PNA alone, e.g. 3'-tailing and (I) may be incorporated into a gene.
CC AAH49208-AAH49264 represent oligonucleotides used to illustrate the
CC method of the invention.

XX
SQ Sequence 18 BP; 0 A; 5 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
|||||
Db 1 gtgtcggggtctccgggc 18

Search completed: October 12, 2002, 17:08:03
Job time: 9/48 sec

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:36 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-5

Perfect score: 18

Sequence: 1 ggtcggtgtctccggc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_NA:*
- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
 - 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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 - 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1	US-08-369-282-1
2	18	100.0	18	1	US-08-445-291-6
C 3	18	100.0	18	1	US-08-445-291-7
4	18	100.0	18	1	US-08-675-120-1
C 5	18	100.0	18	2	US-08-723-052-3
6	18	100.0	18	2	US-08-723-052-4
7	18	100.0	18	3	US-08-578-686C-25
8	18	100.0	18	3	US-09-094-405-13
C 9	18	100.0	18	3	US-09-274-625-3
10	18	100.0	18	3	US-09-274-625-4
C 11	18	100.0	18	3	US-09-274-624-3
12	18	100.0	18	3	US-09-274-624-4
13	18	100.0	18	3	US-09-144-112-25
C 14	18	100.0	18	4	US-09-400-322-3
15	18	100.0	18	4	US-09-400-322-4
16	18	100.0	18	4	US-08-337-120A-13
C 17	18	100.0	18	4	US-09-724-594-3
18	18	100.0	18	4	US-09-724-594-4
19	18	100.0	18	5	PCT-US92-00626-1
20	18	100.0	18	5	PCT-US92-06685-1
21	14.8	82.2	18	1	US-08-369-282-4
22	14.8	82.2	18	1	US-08-462-305-11
23	14.8	82.2	18	2	US-08-613-417A-11
24	14.8	82.2	18	2	US-08-985-583-1
25	14.8	82.2	18	3	US-08-594-452-11
26	14.8	82.2	18	3	US-08-578-686C-10
27	14.8	82.2	18	3	US-09-094-405-12

28	14.8	82.2	18	3	US-09-258-408-11	Sequence 11, Appl
29	14.8	82.2	18	3	US-09-196-132-11	Sequence 11, Appl
30	14.8	82.2	18	3	US-09-144-112-10	Sequence 10, Appl
31	14.8	82.2	18	4	US-09-057-486-3	Sequence 3, Appl
32	14.8	82.2	18	4	US-09-414-872-18	Sequence 18, Appl
33	14.8	82.2	18	4	US-09-078-954-7	Sequence 7, Appl
34	14.8	82.2	18	4	US-08-895-981-11	Sequence 11, Appl
35	14.8	82.2	18	4	US-08-337-120A-12	Sequence 12, Appl
36	14.8	82.2	18	5	PCT-US92-00626-4	Sequence 4, Appl
37	14.8	82.2	18	5	PCT-US92-09656-22	Sequence 22, Appl
38	14.8	82.2	18	5	PCT-US92-09656-26	Sequence 26, Appl
39	14.8	82.2	18	5	PCT-US93-07541-5	Sequence 5, Appl
40	14.8	82.2	18	5	PCT-US93-07541-6	Sequence 6, Appl
41	14.8	82.2	19	4	US-09-414-872-19	Sequence 19, Appl
42	14.8	82.2	19	5	PCT-US92-09656-21	Sequence 21, Appl
43	14.8	82.2	20	5	PCT-US92-09656-20	Sequence 20, Appl
44	14.8	82.2	21	3	US-08-594-452-61	Sequence 61, Appl
45	14.8	82.2	21	3	US-09-258-408-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-08-369-282-1
; Sequence 1, Application US/08369282
; Patent No. 5593974
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, ROBERT D
; APPLICANT: SIMONS, MICHAEL
; APPLICANT: EDELMAN, ELAZER
; APPLICANT: LANGER, ROBERT S
; APPLICANT: DEKEYSER, JEAN-LUC
; TITLE OF INVENTION: LOCALIZED OLIGONUCLEOTIDE THERAPY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,282
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/855,416
; FILING DATE:
; APPLICATION NUMBER: US 792,146
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 723,454
; FILING DATE: 28-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MIT5583CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

ANTI-SENSE: YES
FEATURE: misc.feature
LOCATION: 1-18
OTHER INFORMATION: /standard_name= "ANTISENSE MOUSE"
OTHER INFORMATION: C-MYB
OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO MOUSE C-MYB"
US-08-369-282-1

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 2
US-08-445-291-6
; Sequence 6, Application US/08445291
; Patent No. 5649638
; GENERAL INFORMATION:
; APPLICANT: Polushin, Nikolai N.
; APPLICANT: Efimov, Vladimir A.
; APPLICANT: Morocho, Alan M.
; APPLICANT: Cohen, Jack S.
; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,291
; FILING DATE:
; CLASSIFICATION: 102
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB/J-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-6400
; TELEFAX: (703)836-2787
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-445-291-6

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 3

US-08-445-291-7/c
; Sequence 7, Application US/08445291
; Patent No. 5649638
; GENERAL INFORMATION:
; APPLICANT: Polushin, Nikolai N.
; APPLICANT: Efimov, Vladimir A.
; APPLICANT: Morocho, Alan M.
; APPLICANT: Cohen, Jack S.
; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,291
; FILING DATE:
; CLASSIFICATION: 102
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB/J-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-6400
; TELEFAX: (703)836-2787
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-445-291-7

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
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Db 18 GTGTGGGGGTCTCCGGGC 1

RESULT 4
US-08-675-120-1
; Sequence 1, Application US/08675120
; Patent No. 5679559
; GENERAL INFORMATION:
; APPLICANT: Jin-Seok Kim
; APPLICANT: Atsushi Maruyama
; APPLICANT: Toshihiro Akaike
; APPLICANT: Sung Wan Kim
; TITLE OF INVENTION: CATIONIC POLYMER AND LIPOPROTEIN-
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5679559th & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

COMPUTER: AST Ascentia 900N
OPERATING SYSTEM: DOS 6.22
SOFTWARE: Word Perfect 6.0
CURRENT APPLICATION DATA: US/08/675,120
APPLICATION NUMBER: US/08/675,120
FILING DATE: 03-JUL-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. Howarth
REGISTRATION NUMBER: 36,553
REFERENCE/DOCKET NUMBER: T3622/U-2220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-675-120-1

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 5
US-08-723-052-3/c
; Sequence 3, Application US/08723052
; Patent No. 5922757
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Carson, Dennis
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,052
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Christopher J.
; REGISTRATION NUMBER: 40,179
; REFERENCE/DOCKET NUMBER: UCSD-02424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/705-8410
; TELEFAX: 415/397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-723-052-3

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
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Db 18 GTGTGGGGGTCTCCGGGC 1

RESULT 6
US-08-723-052-4
; Sequence 4, Application US/08723052
; Patent No. 5922757
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Carson, Dennis
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,052
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Christopher J.
; REGISTRATION NUMBER: 40,179
; REFERENCE/DOCKET NUMBER: UCSD-02424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/705-8410
; TELEFAX: 415/397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-723-052-4

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 7
US-08-578-686C-25
; Sequence 25, Application US/08578686C
; Patent No. 6028182
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; TITLE OF INVENTION: Methylphosphonic Acid Ester, Process For
; PREPARING THE SAME AND ITS USE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.

```
; STREET: 1300 I. Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: January 2, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Lori-Ann
; REGISTRATION NUMBER: 34,498
; REFERENCE/DOCKET NUMBER: 2481.1481-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-578-686C-25

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 8
US-09-944-405-13
; Sequence 13, Application US/09094405
; Patent No. 6066720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified oligonucleotides, their preparation
; NUMBER OF SEQUENCES: 30
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,196
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Mous
; FEATURE:
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; NAME/KEY: exon
; LOCATION: 1..18
; OTHER INFORMATION: /note= "c-myb"
; US-09-094-405-13

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18
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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 9
US-09-274-625-3/c
; Sequence 3, Application US/09274625
; Patent No. 6075027
; GENERAL INFORMATION:
; APPLICANT: Choikier, Mario
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; HEPATIC DISORDERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/274,624
; FILING DATE: 23-MAR-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UCSD-03683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/705-8410
; TELEFAX: 415/397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-274-625-3

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcgggggtctccgggc 18
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Db 18 GTGTGGGGGTCTCCGGGC 1

RESULT 10
US-09-274-625-4
; Sequence 4, Application US/09274625
; Patent No. 6075027
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QY 1 gtgtcgggggtctccgggc 18
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Db 1 GTGTGGGGGTCTCCGGGC 18

RESULT 13
US-09-144-112-25
; Sequence 25, Application US/09144112
; Patent No. 6150510
; GENERAL INFORMATION:
; APPLICANT: SEELA, Frank
; APPLICANT: THOMAS, Horst
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES, THEIR PREPARATION AND THEIR
; FILE REFERENCE: 026083/0181
; CURRENT APPLICATION NUMBER: US/09/144,112
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: DE P 44 38 918.3
; PRIOR FILING DATE: 1994-11-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antisense
; OTHER INFORMATION: Oligonucleotide
US-09-144-112-25

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;
QY 1 gtgtcgggggtctccgggc 18
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Db 1 gtgtcgggggtctccgggc 18

RESULT 14
US-09-400-322-3/c
; Sequence 3, Application US/09400322
; Patent No. 6218437
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; FILE REFERENCE: UCSD-03831
; CURRENT APPLICATION NUMBER: US/09/400,322
; CURRENT FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: 08/723,052
; EARLIER FILING DATE: 1996-09-30
; EARLIER APPLICATION NUMBER: 09/274,624
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: 09/274,625
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-400-322-3

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;
QY 1 gtgtcgggggtctccgggc 18

Db 18 GTGTGGGGGTCTCCGGGC 1
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RESULT 15
US-09-400-322-4
; Sequence 4, Application US/09400322
; Patent No. 6218437
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HEPATIC DISORDERS
; FILE REFERENCE: UCSD-03831
; CURRENT APPLICATION NUMBER: US/09/400,322
; CURRENT FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: 08/723,052
; EARLIER FILING DATE: 1996-09-30
; EARLIER APPLICATION NUMBER: 09/274,624
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: 09/274,625
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-400-322-4

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;
QY 1 gtgtcgggggtctccgggc 18
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Db 1 gtgtcgggggtctccgggc 18

Search completed: October 12, 2002, 16:54:37
Job time: 8992 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:31 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-5

Perfect score: 18

Sequence: 1 gtgtcgggggtctccggcg 18

Scoring table: IDENTITY_NUC

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Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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 - 21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq.*
 - 22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq.*
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 - 25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq.*
 - 26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq.*
 - 27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq.*
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 - 34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq.*
 - 35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq.*
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- 46: /cgn2_6/ptodata/2/pna/US6007_COMB.seq.*
- 47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq.*
- 48: /cgn2_6/ptodata/2/pna/US6009_COMB.seq.*
- 49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq.*
- 50: /cgn2_6/ptodata/2/pna/US6011_COMB.seq.*
- 51: /cgn2_6/ptodata/2/pna/US6012_COMB.seq.*
- 52: /cgn2_6/ptodata/2/pna/US6013_COMB.seq.*
- 53: /cgn2_6/ptodata/2/pna/US6014_COMB.seq.*
- 54: /cgn2_6/ptodata/2/pna/US6015_COMB.seq.*
- 55: /cgn2_6/ptodata/2/pna/US6016_COMB.seq.*
- 56: /cgn2_6/ptodata/2/pna/US6017_COMB.seq.*
- 57: /cgn2_6/ptodata/2/pna/US6018_COMB.seq.*
- 58: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
- 59: /cgn2_6/ptodata/2/pna/US6020_COMB.seq.*
- 60: /cgn2_6/ptodata/2/pna/US6021_COMB.seq.*
- 61: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
- 62: /cgn2_6/ptodata/2/pna/US6023_COMB.seq.*
- 63: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
- 64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
- 65: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
- 66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
- 67: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
- 68: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
- 69: /cgn2_6/ptodata/2/pna/US6030_COMB.seq.*
- 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
- 71: /cgn2_6/ptodata/2/pna/US6032_COMB.seq.*
- 72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	1	PCT-US97-12425-1	Sequence 1, Appli
2	18	100.0	18	3	US-07-742-867-1	Sequence 1, Appli
3	18	100.0	18	3	US-07-928-114-1	Sequence 1, Appli
4	18	100.0	18	3	US-07-928-114A-1	Sequence 1, Appli
5	18	100.0	18	5	US-08-145-701-6	Sequence 6, Appli
6	18	100.0	18	5	US-08-145-701-7	Sequence 7, Appli
7	18	100.0	18	7	US-08-318-458A-4	Sequence 4, Appli
8	18	100.0	18	8	US-08-402-838-25	Sequence 25, Appli
9	18	100.0	18	8	US-08-480-216-4	Sequence 4, Appli
10	18	100.0	18	8	US-08-486-490-4	Sequence 4, Appli
11	18	100.0	18	13	US-08-940-196-13	Sequence 13, Appli
12	18	100.0	18	16	US-09-241-561-5	Sequence 5, Appli
13	18	100.0	18	24	US-09-627-787-59	Sequence 59, Appli
14	18	100.0	18	25	US-09-643-233-25	Sequence 25, Appli
15	18	100.0	18	26	US-09-669-187A-661	Sequence 661, App
16	18	100.0	18	29	US-09-724-600-3	Sequence 3, Appli
17	18	100.0	18	29	US-09-724-600-4	Sequence 4, Appli
18	18	100.0	18	29	US-09-724-664-3	Sequence 3, Appli
19	18	100.0	18	29	US-09-724-664-4	Sequence 4, Appli
20	18	100.0	18	29	US-09-724-667-3	Sequence 3, Appli
21	18	100.0	18	29	US-09-724-667-4	Sequence 4, Appli
22	18	100.0	18	29	US-09-724-694-3	Sequence 3, Appli
23	18	100.0	18	29	US-09-724-694-4	Sequence 4, Appli
24	18	100.0	18	29	US-09-724-695-3	Sequence 3, Appli
25	18	100.0	18	29	US-09-724-695-4	Sequence 4, Appli
26	18	100.0	18	29	US-09-724-870-3	Sequence 3, Appli
27	18	100.0	18	29	US-09-724-870-4	Sequence 4, Appli
28	18	100.0	18	30	US-09-793-146-25	Sequence 25, Appli
29	18	100.0	18	32	US-09-835-370-48	Sequence 48, Appli
30	18	100.0	18	32	US-09-835-371-48	Sequence 48, Appli
31	18	100.0	18	33	US-09-888-326-474	Sequence 474, App

Sequence 661, App
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 628, App
Sequence 662, App
Sequence 468, App
Sequence 469, App

ALIGNMENTS

RESULT 1
PCT-US97-12425-1
; Sequence 1, Application PC/TUS9712425
; GENERAL INFORMATION:
; APPLICANT: Jin-Seok Kim
; APPLICANT: Atsushi Maruyama
; APPLICANT: Toshihiro Akaiki
; APPLICANT: Sung Wan Kim
; TITLE OF INVENTION: CATIONIC POLYMER AND LIPOPROTEIN-
; TITLE OF INVENTION: CONTAINING SYSTEM FOR GENE DELIVERY
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, North & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: AST Ascentia 900N
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: Word Perfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12425
; FILING DATE: 03-JUL-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan J. Howarth
; REGISTRATION NUMBER: 36,553
; REFERENCE/DOCKET NUMBER: T3622/U-2220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801)566-6633
; TELEFAX: (801)566-0750
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US97-12425-1

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctcgggc 18
|||||
Db 1 GTGTCTGGGGTCTCGGGC 18

RESULT 2
US-07-742-867-1

Sequence 1, Application US/07742867
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; TITLE OF INVENTION: A Method Of Producing Red Blood Cells
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/742,867
; FILING DATE: 19910809
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: NEDH91-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-742-867-1

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctcgggc 18
|||||
Db 1 GTGTCTGGGGTCTCGGGC 18

RESULT 3
US-928-114-1
; Sequence 1, Application US/07928114
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; TITLE OF INVENTION: A METHOD OF INDUCING HEMOGLOBIN
; TITLE OF INVENTION: SYNTHESIS IN RED BLOOD CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02713
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,114
; FILING DATE: 19920810
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,867

;; FILING DATE: 09-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: NEDH91-05A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-861-6240
;; TELEFAX: 617-861-9540
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-07-928-114-1

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccgggc 18
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Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 4
US-07-928-114A-1
;; Sequence 1, Application US/07928114A
;; GENERAL INFORMATION:
;; APPLICANT: Sytkowski, Arthur J.
;; TITLE OF INVENTION: A METHOD OF INDUCING HEMOGLOBIN
;; SYNTHESIS IN RED BLOOD CELLS
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02713

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US/07/928,114A
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: NEDH91-05A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-928-114A-1

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccgggc 18
|||
Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 5
US-08-145-701-6
;; Sequence 6, Application US/08145701
;; GENERAL INFORMATION:
;; APPLICANT: Polushin, Nikolai N.
;; APPLICANT: Efimov, Vladimir A.
;; APPLICANT: Morcho, Alan M.
;; APPLICANT: Cohen, Jack S.
;; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
;; ANALOGS
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oliff & Berridge
;; STREET: P.O. Box 19928
;; CITY: Alexandria
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB/J-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-6400
TELEFAX: (703)836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-145-701-6

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcggggtctccgggc 18
|||
Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 6
US-08-145-701-7/c
;; Sequence 7, Application US/08145701
;; GENERAL INFORMATION:
;; APPLICANT: Polushin, Nikolai N.
;; APPLICANT: Efimov, Vladimir A.
;; APPLICANT: Morcho, Alan M.
;; APPLICANT: Cohen, Jack S.
;; TITLE OF INVENTION: DEPROTECTION OF OLIGONUCLEOTIDES AND
;; ANALOGS
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oliff & Berridge
;; STREET: P.O. Box 19928
;; CITY: Alexandria
;; STATE: VA

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gtgtcggggtctccgggc 18
Db 18 GTGTCGGGGTCTCCGGGC 1
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,701
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB/J-267
TELEPHONE: (703)836-6400
TELEFAX: (703)836-2787
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-145-701-7

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtgtcggggtctccgggc 18
Db 18 GTGTCGGGGTCTCCGGGC 1

RESULT 7
US-08-318-458A-4
Sequence 4, Application US/08318458A
GENERAL INFORMATION:
APPLICANT: Burgess, Teresa L.
APPLICANT: Farrell, Catherine L.
TITLE OF INVENTION: Method for Inhibiting
TITLE OF INVENTION: Smooth Muscle Cell
TITLE OF INVENTION: Proliferation and
TITLE OF INVENTION: Oligonucleotides for
TITLE OF INVENTION: Use Therein
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Dr.
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.0
SOFTWARE: Microsoft Word Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,458A
FILING DATE: 05OCT1994
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-318-458A-4

Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gtgtcggggtctccgggc 18
Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 8
US-08-402-838-25
Sequence 25, Application US/08402838
GENERAL INFORMATION:
APPLICANT: Uhlmann, Eugen
APPLICANT: Breipohl, Gerhard
TITLE OF INVENTION: Polymide-Oligonucleotide Derivatives,
TITLE OF INVENTION: Their Preparation And Use
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I. Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,838
FILING DATE: 13-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Warnement, Thalia V.
REGISTRATION NUMBER: 39,064
REFERENCE/DOCKET NUMBER: 02481.1437-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-402-838-25

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gtgtcggggtctccgggc 18
Db 1 GTGTCGGGGTCTCCGGGC 18

RESULT 9
US-08-480-216-4
Sequence 4, Application US/08480216
GENERAL INFORMATION:
APPLICANT: Burgess, Teresa L.
APPLICANT: Farrell, Catherine L.
APPLICANT: Fisher, Eric F.
TITLE OF INVENTION: Method for Inhibiting
TITLE OF INVENTION: Smooth Muscle Cell
TITLE OF INVENTION: Proliferation and
US-08-480-216-4

;; TITLE OF INVENTION: Oligonucleotides for
;; TITLE OF INVENTION: Use Therein
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: 1840 Dehavilland Dr.
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: USA
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh OS 7.0
;; SOFTWARE: Microsoft Word Version 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/480,216
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/318,458
;; FILING DATE: 05-OCT-1994
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
US-08-480-216-4

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTCTGGGGTCTCCGGGC 18

RESULT 10
US-08-486-490-4
;; Sequence 4, Application US/08486490
;; GENERAL INFORMATION:
;; APPLICANT: Burgess, Teresa L.
;; APPLICANT: Farrell, Catherine L.
;; APPLICANT: Fisher, Eric F.
;; TITLE OF INVENTION: Method for Inhibiting
;; TITLE OF INVENTION: Smooth Muscle Cell
;; TITLE OF INVENTION: Proliferation and
;; TITLE OF INVENTION: Oligonucleotides for
;; TITLE OF INVENTION: Use Therein
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: 1840 Dehavilland Dr.
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: USA
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh OS 7.0
;; SOFTWARE: Microsoft Word Version 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,490
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/318,458
;; FILING DATE: 05-OCT-1994

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
US-08-486-490-4

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTCTGGGGTCTCCGGGC 18

RESULT 11
US-08-940-196-13
;; Sequence 13, Application US/08940196
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Modified oligonucleotides, their preparation
;; TITLE OF INVENTION: and use
;; NUMBER OF SEQUENCES: 30
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA: US/08/940,196
;; FILING DATE:
;; CLASSIFICATION: 536
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Mous
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 1..18
;; OTHER INFORMATION: /note= "c-myb"
US-08-940-196-13

Query Match 100.0%; Score 18; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
| | | | | | | | | | | | | | | | | |
Db 1 GTGTCTGGGGTCTCCGGGC 18

RESULT 12
US-09-241-561-5
;; Sequence 5, Application US/09241561
;; GENERAL INFORMATION:
;; APPLICANT: SIROIS, Martin G.
;; APPLICANT: EDELMAN, Elazer R.
;; APPLICANT: ROSENBERG, Robert D.
;; APPLICANT: SIMONS, Michael
;; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
;; TITLE OF INVENTION: Restenosis

Search completed: October 12, 2002, 20:42:31
Job time: 16401 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:27:30 ; Search time 1154.93 Seconds
(without alignments)
52.829 Million cell updates/sec

Title: US-09-945-131-5
Perfect score: 18
Sequence: 1 gtgtcgggggtctccgggc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2385415 seqs, 1694839300 residues

Total number of hits satisfying chosen parameters: 1365168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
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3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
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7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	18	100.0	18	5	US-09-945-131-5
2	18	100.0	18	5	US-09-945-166A-6
3	18	100.0	18	5	US-09-945-166A-7
4	18	100.0	18	5	US-09-776-479-661
5	18	100.0	18	7	US-10-112-653-634
6	16.4	91.1	18	5	US-09-776-479-628
7	16.4	91.1	18	5	US-09-776-479-662
8	16.4	91.1	18	7	US-10-112-653-604
9	16.4	91.1	18	7	US-10-112-653-635
10	14.8	82.2	18	5	US-09-315-298C-9
11	13.8	76.7	30	1	PCT-US02-05625-34
12	13.4	74.4	50	5	US-09-718-321A-1058
13	12.6	70.0	15	1	PCT-US02-14004-18
14	12.4	68.9	25	5	US-09-396-196G-24964
15	12.4	68.9	25	6	US-10-215-112-2404
16	12.2	67.8	24	5	US-09-852-416-18
17	12.2	67.8	25	5	US-09-396-196G-61672
18	12.2	67.8	40	1	PCT-US02-25940-9670
19	12	66.7	13	5	US-09-509-152C-1893
20	12	66.7	14	5	US-09-509-152C-1894
21	12	66.7	15	5	US-09-509-152C-1442
22	12	66.7	18	5	US-09-509-152C-1368
23	11.8	65.6	25	5	US-09-956-604-104106
24	11.8	65.6	25	5	US-09-956-604-123889
25	11.8	65.6	25	5	US-09-396-196G-114792

c	26	11.8	65.6	44	1	PCT-US01-47994-11	Sequence 11, Appl
c	27	11.8	65.6	44	1	PCT-US01-47994-12	Sequence 12, Appl
c	28	11.6	64.4	20	1	PCT-US02-25940-14621	Sequence 14621, A
c	29	11.6	64.4	20	1	PCT-US02-25940-14622	Sequence 14622, A
c	30	11.6	64.4	20	5	US-09-858-152A-6	Sequence 6, Appl
c	31	11.6	64.4	25	5	US-09-396-196G-35792	Sequence 35792, A
c	32	11.6	64.4	25	5	US-09-396-196G-35793	Sequence 35793, A
c	33	11.6	64.4	29	7	US-10-913-970-12	Sequence 12, Appl
c	34	11.6	64.4	38	5	US-09-745-237A-2930	Sequence 2930, Ap
c	35	11.6	64.4	38	5	US-09-745-237A-2940	Sequence 2940, Ap
c	36	11.6	64.4	38	5	US-09-745-237A-3074	Sequence 3074, Ap
c	37	11.6	64.4	38	5	US-09-745-237A-3086	Sequence 3086, Ap
c	38	11.6	64.4	38	5	US-09-745-237A-3099	Sequence 3099, Ap
c	39	11.6	64.4	38	5	US-09-745-237A-3102	Sequence 3102, Ap
c	40	11.6	64.4	40	6	US-10-208-304-9	Sequence 9, Appl
c	41	11.6	64.4	41	1	PCT-US02-25943-31780	Sequence 31780, A
c	42	11.6	64.4	47	7	US-10-170-097-1163	Sequence 1163, Ap
c	43	11.4	63.3	15	1	PCT-US02-25940-1165	Sequence 1165, Ap
c	44	11.4	63.3	15	1	PCT-US02-25940-15037	Sequence 15037, A
c	45	11.4	63.3	17	7	US-10-156-306-5937	Sequence 5937, Ap

ALIGNMENTS

RESULT 1
US-09-945-131-5
; Sequence 5, Application US/09945131
; GENERAL INFORMATION:
; APPLICANT: SIROIS, Martin G.
; APPLICANT: EDELMAN, Elazer R.
; APPLICANT: ROSENBERG, Robert D.
; APPLICANT: SIMONS, Michael
; TITLE OF INVENTION: Localized Oligonucleotide Therapy for Preventing
; FILE REFERENCE: 12554.4
; CURRENT APPLICATION NUMBER: US/09/945,131
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/241,561
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,554
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(18)
; OTHER INFORMATION: Antisense oligonucleotide
US-09-945-131-5

Query Match 100.0% Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtcgggggtctccgggc 18
Db 1 gtgtcgggggtctccgggc 18

RESULT 2
US-09-945-166A-6
; Sequence 6, Application US/09945166A
; GENERAL INFORMATION:
; APPLICANT: ELMALEH, DAVID R.
; APPLICANT: FISCHMAN, ALAN J.
; APPLICANT: BABICH, JOHN W.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID CONSTRUCTS AND USES RELATED
; TITLE OF INVENTION: THERETO

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; FILE REFERENCE: MGA-003.01
; CURRENT APPLICATION NUMBER: US/09/945,166A
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-945-166A-6
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Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 gtgtcggggtctccgggc 18
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RESULT 3

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US-09-945-166A-7/c
; Sequence 7, Application US/09945166A
; GENERAL INFORMATION:
; APPLICANT: ELMALEH, DAVID R.
; APPLICANT: FISCHMAN, ALAN J.
; APPLICANT: BABICH, JOHN W.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID CONSTRUCTS AND USES RELATED
; FILE OF INVENTION: THERETO
; FILE REFERENCE: MGA-003.01
; CURRENT APPLICATION NUMBER: US/09/945,166A
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-945-166A-7
```

```
Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 gtgtcggggtctccgggc 18
Db 18 GTGTGGGGTCTCCGGGC 1
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RESULT 4

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US-09-776-479-661
; Sequence 661, Application US/09776479
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
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```
; SEQ ID NO 661
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-661
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```
Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 gtgtcggggtctccgggc 18
Db 1 gtgtcggggtctccgggc 18
|||||
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RESULT 5

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US-10-112-653-634
; Sequence 634, Application US/10112653
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 634
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-634
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Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 gtgtcggggtctccgggc 18
Db 1 gtgtcggggtctccgggc 18
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RESULT 6

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US-09-776-479-628
; Sequence 628, Application US/09776479
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 628
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
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Query Match 91.1%; Score 16.4; DB 7; Length 18;
Best Local Similarity 94.4%;
Matches 17; Conservative 0; Mismatches 1; Indels
Pred. No. 3.6e+02;

RESULT 11
PCT-US02-05625-34/c
; Sequence 34, Application PC/TUS0205625
; GENERAL INFORMATION:
; APPLICANT: Arena Pharmaceuticals, Inc.
; TITLE OF INVENTION: Endogenous And Non-Endogenous, Constitutively Activated G Protein
; FILE REFERENCE: AREN-0321
; CURRENT APPLICATION NUMBER: PCT/US02/05625
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Novel Sequence
PCT-US02-05625-34

Query Match 76.7%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gtctcgggggtctccggg 17
||| ||||| |||||
Db 23 GTCTCGGGGGCTCCGGG 7

RESULT 12
US-09-718-321A-1058/c
; Sequence 1058, Application US/09718321A
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/09/718,321A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/163,783
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 1058
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; FEATURE:
; OTHER INFORMATION: single nucleotide polymorphism
; NAME/KEY: misc feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43135797
US-09-718-321A-1058

Query Match 74.4%; Score 13.4; DB 5; Length 50;
Best Local Similarity 93.3%; Pred. No. 7.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gtctcgggggtctccggg 17
||| ||||| |||||
Db 26 GTCCGGGGTCTCCGGG 12

RESULT 13
PCT-US02-14004-18
; Sequence 18, Application PC/TUS0214004
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshy, Beena
; APPLICANT: Rounds, Eileen
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRB GENE
; FILE REFERENCE: MMH-0480PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14004
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/287,960
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14004-18

Query Match 70.0%; Score 12.6; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2e+04; 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 tgtcgggggtctcc 14
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Db 1 tgtcgggkctcc 13

RESULT 14
US-09-396-1966G-24964/c
; Sequence 24964, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Afymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24964
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-1966G-24964

Query Match 68.9%; Score 12.4; DB 5; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 cggggtctccgggc 18
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Db 14 CGGGGTCTCTCTGC 1

RESULT 15
US-10-215-112-2404/c
; Sequence 2404, Application US/10215112
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:

; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2404

Query Match 68.9%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gtcggggtctccgg 16
||||| |||||
Db 14 GTCGGGGCTCCGG 1

Search completed: October 12, 2002, 17:27:31
Job time: 10806 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:03 ; Search time 792.17 Seconds
(without alignments)
39.012 Million cell updates/sec

Title: US-09-945-131-6

Perfect score: 18

Sequence: 1 catgtctccacacttga 18

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-n-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-n-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	14	AAQ42218
2	18	100.0	18	14	AAQ34767
3	18	100.0	18	21	AAAL3832
4	14.8	82.2	30	18	AAT43352
5	14.8	82.2	30	18	AAT43356
6	14.8	82.2	34	18	AAT43354
7	14.8	82.2	36	21	AAA35676
8	13.8	76.7	41	18	AAT93540
9	13.8	76.7	41	19	AAV18847

C 10	13.8	76.7	41	20	AAH78449
C 11	13.4	74.4	23	22	AAF69745
C 12	13.2	73.3	20	21	AAZ34849
C 13	13.2	73.3	20	21	AAZ34797
C 14	13.2	73.3	24	22	AAH19003
C 15	13.2	73.3	24	22	AAH19025
C 16	13.2	73.3	28	22	AAF80037
C 17	13.2	73.3	30	20	AAH19510
C 18	13.2	73.3	36	22	AAF31157
C 19	13.2	73.3	36	22	AAF31158
C 20	13.2	73.3	50	21	AAH53009
C 21	13.2	73.3	50	21	AAH53010
C 22	12.8	71.1	22	21	AAZ88926
C 23	12.8	71.1	23	20	AAZ09332
C 24	12.8	71.1	24	20	AAZ09347
C 25	12.8	71.1	25	21	AAH10590
C 26	12.8	71.1	29	21	AAH76231
C 27	12.8	71.1	33	19	AAV71008
C 28	12.8	71.1	33	21	AAH00051
C 29	12.8	71.1	35	17	AAT36519
C 30	12.8	71.1	37	15	AAQ69217
C 31	12.8	71.1	45	21	AAH58499
C 32	12.8	71.1	45	21	AAH37213
C 33	12.8	71.1	45	22	AAH54319
C 34	12.8	71.1	48	23	ABK09114
C 35	12.8	71.1	49	19	AAV30374
C 36	12.4	68.9	18	21	AAH53246
C 37	12.4	68.9	20	20	AAZ05992
C 38	12.4	68.9	23	20	AAH24437
C 39	12.4	68.9	27	21	AAH36366
C 40	12.4	68.9	29	21	AAH88022
C 41	12.4	68.9	45	16	AAQ94195
C 42	12.4	68.9	45	16	AAQ94196
C 43	12.4	68.9	45	21	AAH53225
C 44	12.4	68.9	45	21	AAH88934
C 45	12.4	68.9	50	11	AAQ06701

ALIGNMENTS

RESULT 1
AAQ42218
ID AAQ42218 standard; DNA; 18 BP.
XX AAQ42218;
AC AAQ42218;
XX
DT 02-SEP-1993 (first entry)
XX Antisense sequence to human NMHC.
DE Antisense; oligonucleotide; inhibit; translation; transcription;
KW target; nucleic acid; mammal; tissue; hybridise; combine; carrier;
KW polyethylene oxide; polypropylene oxide; copolymer; ss.
XX
OS Synthetic.
XX
PN WO9308845-A.
XX
PD 13-MAY-1993.
XX
PF 05-NOV-1992; 92WO-US09626.
XX
PR 08-NOV-1991; 91US-0792146.
PR 18-MAR-1992; 92US-0855416.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
PI Simons M;
XX
DR WPI; 1993-167406/20.
XX

HIV gag gene (QSRN)
Human IL4RALpha ge
Feline CTLA-4 3' p
Cat CTLA-4 recepto
Reverse primer use
Reverse primer use
PCR primer used to
Human lipocalin ho
Mutagenic primer #
Mutagenic primer #
Aspergillus niger
Aspergillus niger
Hepatitis B virus
Synthetic liposam
Pseudomonas sp. st
Probe specific for
E. coli Argu trna
PCR primer Smad2-t
Smad2-top PCR prim
Primer to amplify
PCR primer C3633CC
Human PRO1283 (UNQ
Human PRO1283 hydr
Probe #26 used in
Human CD20 Amberzy
Oligomer p49rg12 u
P450 polymorphism
PCR primer used to
CAT CTLA4 downstre
PCR primer Guava-u
Human neuroblastom
Transmembrane olig
Transmembrane olig
Human G-protein co
Hepatitis B virus
:HBV.LLA2C.56 ampl

PT Inhibiting translation or transcription of target nucleic acid -
PT by local administration in vivo of oligo:nucleotide complementary
PT to target sequence
XX
PS Disclosure; Page 40; 65pp; English.
XX
CC The sequences given in AAQ42217-21 are antisense oligonucleotides
CC which were used to inhibit translation or transcription of target
CC nucleic acids at a locus in vivo. The oligonucleotide are applied
CC directly to a tissue at the locus within the body of a mammal and
CC they are able to penetrate the cells of the tissue, hybridise/combine
CC with the target nucleic acid inhibiting intracellular translation or
CC transcription. The oligonucleotide are incorporated into a carrier
CC eg. a polyethylene oxide-polypropylene oxide copolymer.
XX
SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
Db 1 catgtctccaccttga 18

RESULT 2
AAQ34767
ID AAQ34767 standard; DNA; 18 BP.
XX
AC AAQ34767;
XX
DT 02-JUN-1993 (first entry)
XX
DE Nonmuscle myosin (NMHC) antisense oligonucleotide.
XX
KW Antisense; inhibit; protein coding genes; regulatory DNA; stroke;
KW endonuclease; vascular restenosis; myocardial infarction; embolism;
KW peripheral muscular disease; peripheral angioplasty; thrombophlebitis;
KW vasculitis; angina; Budd-Chiari syndrome; thrombosis; atherosclerosis;
KW hypertension; primary pulmonary; proliferative glomerulonephritis;
KW acute respiratory distress syndrome; idiopathic pulmonary fibrosis;
KW emphysema; ss.
XX
OS Synthetic.
XX
PN WO9301286-A.
XX
PD 21-JAN-1993.
XX
PF 23-JUN-1992; 92WO-0505305.
XX
PR 28-JUN-1991; 91US-0723454.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
PI Simons M;
XX
XX WPI; 1993-045491/05.
XX
XX Localised therapy using anti-sense oligo:nucleotide(s) - which
XX penetrate through tissue cell to hybridise with target m-RNA and
XX inhibit expression of the gene, for treatment of vascular
XX disorders, atherosclerosis, hypertension, etc.
XX
PS Disclosure; Page 21; 59pp; English.
XX
CC The sequences given in AAQ34766-67 and AAQ35258-60 are antisense
CC oligonucleotides which were used in a method of inhibiting a target
CC nucleic acid sequence. The method may be used for inhibiting the
CC expression of protein coding genes as well as regulatory DNA.

CC Application of the antisense oligonucleotides to a defined locus in
CC vivo allows their use when systemic administration is not possible,
CC ie. systemically administered oligos may be rendered inefficient by
CC endonucleases before they reach their targets. This method may be
CC used in the treatment of vascular disorders, particularly vascular
CC restenosis, myocardial infarction, peripheral muscular disease;
CC peripheral angioplasty, thrombophlebitis, stroke, embolism,
CC vasculitis, angina, Budd-Chiari syndrome, thrombosis, atherosclerosis,
CC hypertension, primary pulmonary hypertension, proliferative glomerulo-
CC nephritis, acute respiratory distress syndrome, idiopathic pulmonary
CC fibrosis or emphysema.
XX
SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtctccaccttga 18
Db 1 catgtctccaccttga 18

RESULT 3
AAAL3832
ID AAAL3832 standard; DNA; 18 BP.
XX
AC AAAL3832;
XX
DT 27-JUL-2000 (first entry)
XX
DE NMHC phosphorothioate antisense oligonucleotide SEQ ID NO:6.
XX
KW Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW recurrent stenosis; cardiovascular injury; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
XX CA2228977-A1.
XX
XX 07-MAY-1999.
XX
XX 03-FEB-1998; 98CA-2228977.
XX
XX 07-NOV-1997; 97CA-2215360.
XX
XX (EDEL/) EDELMAN E R.
XX (ROSE/) ROSENBERG R D.
XX (SIRO/) SIROIS M G.
XX (SIMO/) SIMONS M.
XX
XX Edelman ER, Rosenberg RD, Siros MG, Simons M;
XX WPI; 2000-283933/25.
XX
XX Antisense inhibition of platelet derived growth factor beta-receptor
XX subunit expression for the prevention of restenosis -
XX Claim 27; Page 23; 43pp; English.
XX
XX A method has been developed for preventing restenosis following vascular
XX injury by antisense inhibition of platelet derived growth factor
XX beta-receptor subunit (PDGFR-beta) expression. The method is used for
XX the prevention of restenosis (recurrent stenosis (narrowing of a duct or
XX canal), especially of a valve in the heart, after surgical correction of
XX the primary condition) following cardiovascular injury. The present

CC sequence represents a phosphorothioate antisense oligonucleotide for
 CC NMHC.

XX Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 other;

SQ Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 catgtctccacccttga 18
 ||||| ||||| ||||| |||||
 Db 1 catgtctccacccttga 18

RESULT 4

AAAT43352
 ID AAAT43352 standard; cDNA; 30 BP.

XX AC AAAT43352;

XX DT 08-SEP-1997 (first entry)

XX DE Primer #1 for G-protein coupled receptor coding sequence.

XX KW G-protein coupled receptor; human; HIBEF51; transmembrane domain; ulcer;
 KW hormone; viral receptor; growth factor; neuroreceptor; neurotransmitter;
 KW signal transduction; central nervous system; hypertension; osteoporosis;
 KW angina pectoris; myocardial infarction; asthma; allergy; eating disorder;
 KW psychosis; depression; migraine; vomiting; stroke; cancer; hypotension;
 KW benign hypertrophy; Parkinson's disease; acute heart failure; therapy;
 KW urinary retention; primer; polymerase chain reaction; amplify; PCR; ss.

XX OS Synthetic.

XX PN WO9639441-A1.

XX PD 12-DEC-1996.

XX PF 06-JUN-1995; 95WO-US07225.

XX PR 06-JUN-1995; 95WO-US07225.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Adams MD, Li Y;

XX DR WPI; 1997-043076/04.

XX Human G-protein coupled receptor, HIBEF51 - used to identify
 PT (ant)agonists, used in the treatment of asthma, angina pectoris,
 PT psychotic and neurological disorders, and eating disorders etc.

XX Example 1; Page 35; 69pp; English.

XX AAAT43352-T43357 represent primers for the coding sequence for the human
 CC G-protein coupled receptor HIBEF51 (see AAAT43351 for amplified
 CC sequence). The protein encoded by the amplified sequence is a
 CC 7-transmembrane domain receptor. G-protein coupled receptors include a
 CC wide range of biologically active receptors, such as hormone, viral,
 CC growth factor and neuroreceptors. Most of the receptors have conserved
 CC cysteine residues in the first two extracellular loops, which form
 CC disulphide bonds thought to stabilise the functional protein structure.
 CC Phosphorylation or lipidation of these residues can influence the signal
 CC transduction of some G-protein coupled receptors. G-protein coupled
 CC receptors are found at numerous sites within a mammalian host, and some
 CC are critical neurotransmitters in the central nervous system. Compounds
 CC that activate or inhibit the receptor encoded by the amplified sequence
 CC may be used for the treatment of patients which need to activate or
 CC inhibit a G-protein coupled receptor. Mutations in the amplified sequence
 CC or the encoded protein may be identified by sequence analysis.
 CC Antagonists of the G-protein coupled receptor may be used for the
 CC treatment of hypertension, angina pectoris, myocardial infarction,

CC ulcers, asthma, allergies, psychoses, depression, migraine, vomiting,
 CC stroke, eating disorders, cancer and benign hypertrophy. Agonists of the
 CC protein may be used in the treatment of Parkinson's disease, acute heart
 CC failure, hypotension, urinary retention and osteoporosis.

XX SQ Sequence 30 BP; 7 A; 10 C; 5 G; 8 T; 0 other;

Query Match 82.2%; Score 14.8; DB 18; Length 30;
 Best Local Similarity 88.9%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 catgtctccacccttga 18
 ||||| ||||| ||||| |||||
 Db 12 catgaactccacccttga 29

RESULT 5

AAAT43356
 ID AAAT43356 standard; cDNA; 30 BP.

XX AC AAAT43356;

XX DT 09-SEP-1997 (first entry)

XX DE Primer #5 for G-protein coupled receptor coding sequence.

XX KW G-protein coupled receptor; human; HIBEF51; transmembrane domain; ulcer;
 KW hormone; viral receptor; growth factor; neuroreceptor; neurotransmitter;
 KW signal transduction; central nervous system; hypertension; osteoporosis;
 KW angina pectoris; myocardial infarction; asthma; allergy; eating disorder;
 KW psychosis; depression; migraine; vomiting; stroke; cancer; hypotension;
 KW benign hypertrophy; Parkinson's disease; acute heart failure; therapy;
 KW urinary retention; primer; polymerase chain reaction; amplify; PCR; ss.

XX OS Synthetic.

XX PN WO9639441-A1.

XX PD 12-DEC-1996.

XX PF 06-JUN-1995; 95WO-US07225.

XX PR 06-JUN-1995; 95WO-US07225.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Adams MD, Li Y;

XX DR WPI; 1997-043076/04.

XX Human G-protein coupled receptor, HIBEF51 - used to identify
 PT (ant)agonists, used in the treatment of asthma, angina pectoris,
 PT psychotic and neurological disorders, and eating disorders etc.

XX Example 3; Page 38; 69pp; English.

XX AAAT43352-T43357 represent primers for the coding sequence for the human
 CC G-protein coupled receptor HIBEF51 (see AAAT43351 for amplified
 CC sequence). The protein encoded by the amplified sequence is a
 CC 7-transmembrane domain receptor. G-protein coupled receptors include a
 CC wide range of biologically active receptors, such as hormone, viral,
 CC growth factor and neuroreceptors. Most of the receptors have conserved
 CC cysteine residues in the first two extracellular loops, which form
 CC disulphide bonds thought to stabilise the functional protein structure.
 CC Phosphorylation or lipidation of these residues can influence the signal
 CC transduction of some G-protein coupled receptors. G-protein coupled
 CC receptors are found at numerous sites within a mammalian host, and some
 CC are critical neurotransmitters in the central nervous system. Compounds
 CC that activate or inhibit the receptor encoded by the amplified sequence
 CC may be used for the treatment of patients which need to activate or
 CC inhibit a G-protein coupled receptor. Mutations in the amplified sequence
 CC or the encoded protein may be identified by sequence analysis.

CC Antagonists of the G-protein coupled receptor may be used for the
 CC treatment of hypertension, angina pectoris, myocardial infarction,
 CC ulcers, asthma, allergies, psychoses, depression, migraine, vomiting,
 CC stroke, eating disorders, cancer and benign hypertrophy. Agonists of the
 CC protein may be used in the treatment of Parkinson's disease, acute heart
 CC failure, hypotension, urinary retention and osteoporosis.
 CC
 XX Sequence 30 BP; 6 A; 11 C; 6 G; 7 T; 0 other;
 SQ

Query Match 82.2%; Score 14.8; DB 18; Length 30;
 Best Local Similarity 88.9%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
 |||| |||||
 Db 12 catgaactccaccttga 29

RESULT 6
 AAT43354
 ID AAT43354 standard; cDNA; 34 BP.
 XX
 AC AAT43354;
 XX
 DT 09-SEP-1997 (first entry)
 XX
 DE Primer #3 for G-protein coupled receptor coding sequence.
 XX
 KW G-protein coupled receptor; human; HIBEF51; transmembrane domain; ulcer;
 KW hormone; viral receptor; growth factor; neuroreceptor; neurotransmitter;
 KW signal transduction; central nervous system; hypertension; osteoporosis;
 KW angina pectoris; myocardial infarction; asthma; allergy; eating disorder;
 KW psychoses; depression; migraine; vomiting; stroke; cancer; hypotension;
 KW benign hypertrophy; Parkinson's disease; acute heart failure; therapy;
 KW urinary retention; primer; polymerase chain reaction; amplify; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9639441-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 06-JUN-1995; 95WO-US07225.
 XX
 PR 06-JUN-1995; 95WO-US07225.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Adams MD, Li Y;
 XX
 DR WPI; 1997-043076/04.
 XX
 PT Human G-protein coupled receptor, HIBEF51 - used to identify
 PT (ant)agonists, used in the treatment of asthma, angina pectoris,
 PT psychotic and neurological disorders, and eating disorders etc.
 XX
 PS Example 2; Page 37; 69pp; English.
 XX
 CC AAT43352-T43357 represent primers for the coding sequence for the human
 CC G-protein coupled receptor HIBEF51 (see AAT43351 for amplified
 CC sequence). The protein encoded by the amplified sequence is a
 CC 7-transmembrane domain receptor. G-protein coupled receptors include a
 CC wide range of biologically active receptors, such as hormone, viral,
 CC growth factor and neuroreceptors. Most of the receptors have conserved
 CC cysteine residues in the first two extracellular loops, which form
 CC disulphide bonds thought to stabilise the functional protein structure.
 CC Phosphorylation or lipidation of these residues can influence the signal
 CC transduction of some G-protein coupled receptors. G-protein coupled
 CC receptors are found at numerous sites within a mammalian host, and some
 CC are critical neurotransmitters in the central nervous system. Compounds
 CC that activate or inhibit the receptor encoded by the amplified sequence
 CC may be used for the treatment of patients which need to activate or

CC inhibit a G-protein coupled receptor. Mutations in the amplified sequence
 CC or the encoded protein may be identified by sequence analysis.
 CC Antagonists of the G-protein coupled receptor may be used for the
 CC treatment of hypertension, angina pectoris, myocardial infarction,
 CC ulcers, asthma, allergies, psychoses, depression, migraine, vomiting,
 CC stroke, eating disorders, cancer and benign hypertrophy. Agonists of the
 CC protein may be used in the treatment of Parkinson's disease, acute heart
 CC failure, hypotension, urinary retention and osteoporosis.
 CC
 XX Sequence 34 BP; 8 A; 12 C; 6 G; 8 T; 0 other;
 SQ

Query Match 82.2%; Score 14.8; DB 18; Length 34;
 Best Local Similarity 88.9%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttga 18
 |||| |||||
 Db 16 catgaactccaccttga 33

RESULT 7
 AAA35676
 ID AAA35676 standard; DNA; 36 BP.
 XX
 AC AAA35676;
 XX
 DT 26-JUL-2000 (first entry)
 XX
 DE Permutin linker encoding nucleotide sequence FGS101.
 XX
 KW Biologically-activated circularly-permuted protein; permutin; linker;
 KW permutin library generation; therapeutic property; antigen;
 KW immunotherapy; improve bio-distribution; half life; ss.
 XX
 OS Synthetic.
 XX
 PN WO200018905-A1.
 XX
 PD 06-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US20891.
 XX
 PR 25-SEP-1998; 98US-0101908.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Lee SC;
 XX
 DR WPI; 2000-293145/25.
 XX
 PT Preparation of biologically-activated circularly-permuted proteins by
 PT scanning permutagenesis for generating libraries of permutins with
 PT improved therapeutic properties -
 PS Claim 11; Page 41; 100pp; English.
 XX
 CC The preparation of biologically-activated circularly-permuted proteins
 CC (permutins) comprises the use of a method comprising making a series of
 CC circularly permuted genes. The circularly permuted genes are inserted
 CC into a display vector, where they are expressed so that the proteins
 CC they encode are presented on the surface of the display vector. A library
 CC of display vectors presenting the expressed circularly permuted proteins
 CC is generated. A target protein that can bind a biologically active
 CC circularly permuted protein can be used to affinity select the
 CC presenting display vectors. The selected circularly-permuted protein. The
 CC and analysed to identify the structure of a parent protein consisting of a
 CC permutin derived from the carboxy terminus of the parent protein, and a
 CC segment derived from the amino terminus of the parent protein, and a
 CC linker or chemical bond linking the amino and carboxy terminal derived
 CC portions. Nucleotide sequences AAA35676-A35943 encode linkers used to
 CC create the permutins of the invention. The method is used to generate

CC libraries of permuteins with improved therapeutic properties compared to
 CC their parent molecules. Permutoins with little or no activity may be used
 CC as antigens for producing antibodies which are used in immunology or
 CC immunotherapy as probes or intermediates used to construct other useful
 CC permutoins. Permutoins have improved biological and therapeutic
 CC properties compared to their two individual components due to alterations
 CC in bio-distribution or half-life.

XX Sequence 36 BP; 7 A; 15 C; 8 G; 6 T; 0 other;

Query Match 82.2%; Score 14.8; DB 21; Length 36;
 Best Local Similarity 88.9%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtctccacacttggg 18
 ||||| ||||| |||||
 Db 9 catgtctccacacttggg 26

RESULT 8
 AAT93540/C
 ID AAT93540 standard; DNA; 41 BP.

XX AAT93540;

XX 19-FEB-1998 (first entry)

DE Antisense primer SK462 for amplification of QS RNA.

XX Armoured RNA; bacteriophage MS2; RT-PCR; ribonuclease; recombinant;
 KW Human Immunodeficiency Virus; HIV; Hepatitis C Virus; HCV; viral RNA;
 KW detection; quantification standard; maturase protein; coat protein;
 KW PCR primer; QS RNA; reverse transcriptase-PCR; ss.

XX Synthetic.

OS Human Immunodeficiency Virus.

XX US5677124-A.

XX 14-OCT-1997.

XX 03-JUL-1996; 96US-0675153.

XX 03-JUL-1996; 96US-0675153.

XX (AMBI-) AMBION INC.

PA (CENE-) CENETRON DIAGNOSTICS LLC.

XX Dubois DB, Pasloske BL, Winkler MM;

DR WPI; 1997-511866/47.

XX Recombinant RNA segment encapsidated in bacteriophage viral coat
 PT protein - RNA detection and/or quantification standard

XX Example 1; Column 15; 23pp; English.

CC This antisense primer is used in the RT-PCR amplification of QS RNA. The
 CC QS RNA is used to construct an "armoured RNA" HIV standard PAR-2. An
 CC "armoured RNA" is a recombinant RNA segment encapsidated in bacteriophage
 CC viral coat protein. The recombinant RNA segment comprises an operator
 CC coding sequence, a viral maturase protein binding site, and a non-
 CC bacteriophage sequence. The QS sequence is the non bacteriophage HIV
 CC standard in this case. The recombinant RNA in its packaged form is highly
 CC resistant to ribonucleases, insuring that the RNA standard is not
 CC compromised by inadvertent ribonuclease contamination. The armoured RNA
 CC standards are ideal as RNA standards for the quantification of RNA
 CC viruses such as HIV and HCV from human body fluids such as blood and
 CC cerebrospinal fluid.

XX Sequence 41 BP; 15 A; 7 C; 10 G; 9 T; 0 other;

Query Match 76.7%; Score 13.8; DB 18; Length 41;
 Best Local Similarity 88.2%; Pred. No. 1.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacacttggg 18
 ||||| ||||| |||||
 Db 24 ATGTCTCTCCCACTTAGA 8

RESULT 9
 AAV18847/C

ID AAV18847 standard; DNA; 41 BP.

XX AAV18847;

XX 11-JUN-1998 (first entry)

DE Primer for QS RNA.

XX PCR primer; QS RNA; nucleic acid standard;
 KW Armored RNA; ss.

XX Synthetic.

XX WO9800547-A1.

XX 08-JAN-1998.

XX 02-JUL-1997; 97WO-US12551.

XX 24-JUN-1997; 97US-0881571.

XX 03-JUL-1996; 96US-0021145.

XX 03-JUL-1996; 96US-0675153.

XX (AMBI-) AMBION INC.

PA (CENE-) CENETRON DIAGNOSTICS LLC.

XX Dubois DB, Pasloske BL, Winkler MM;

XX WPI; 1998-086972/08.

XX Ribonuclease resistant RNA molecules and their production - useful
 PT as standards in quantitative PCR for pathogens, e.g HIV-1, HIV-2 and
 PT HCV

XX Example 1; Page 32; 134pp; English.

XX The present sequence is a primer for QS RNA, which was used in the
 CC preparation of a nucleic acid standard, comprising a nuclease
 CC resistant nucleic acid segment encoding a standard nucleic acid,
 CC i.e. RNA. The ribonuclease resistant RNA standard, designated
 CC Armored RNA (RTM) is useful as an internal or external nucleic acid
 CC standard in quantitative assays, e.g. PCR or RT-PCR for the
 CC presence of a tested nucleic acid in blood samples.

XX Sequence 41 BP; 15 A; 7 C; 10 G; 9 T; 0 other;

Query Match 76.7%; Score 13.8; DB 19; Length 41;
 Best Local Similarity 88.2%; Pred. No. 1.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctccacacttggg 18
 ||||| ||||| |||||
 Db 24 ATGTCTCTCCCACTTAGA 8

RESULT 10
 AAX78449/C

ID AAX78449 standard; DNA; 41 BP.

XX AAX78449;

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XX DT 26-AUG-1999 (first entry)
XX DE HIV gag gene (QSRNA) PCR primer 2.
XX DE RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
XX KW ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV;
XX KW HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.
XX OS Synthetic.
XX OS Human immunodeficiency virus.
XX PN US5919625-A.
XX PD 06-JUL-1999.
XX PF 29-APR-1997; 97US-0841252.
XX PR 03-JUL-1996; 96US-0675153.
XX PR 29-APR-1997; 97US-0841252.
XX PA (AMBI-) AMBION INC.
XX PA (GENE-) CENTRON DIAGNOSTICS LLC.
XX PI Dubois DB, Pasloske BL, Winkler MW;
XX DR WPI; 1999-394617/33.
XX XX Ribonuclease resistant viral RNA standards
XX PT Example 1; Column 29-30; 22pp; English.
XX XX This invention describes the construction of novel RNA standards for the
XX CC quantification of human immunodeficiency virus (HIV) and hepatitis C
XX CC virus (HCV) from e.g. cerebrospinal fluids. The method involves (1)
XX CC obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
XX CC RNA standard, encapsulated in a bacteriophage viral coat protein, which
XX CC comprises an RNA segment having a segment encoding a sequence that serves
XX CC as a standard in detection or quantification of the RNA of interest;
XX CC (3) mixing the sample with the standard; (4) isolating RNA from the
XX CC mixture, and (5) assaying for the presence of the RNA. The method is
XX CC useful for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1,
XX CC HTLV-2, hepatitis G, an enterovirus, or a blood-borne pathogen. This
XX CC sequence represents a PCR primer used to amplify the HIV gag gene QSRNA
XX CC which is used in the method of the invention.
XX SQ Sequence 41 BP; 15 A; 7 C; 10 G; 9 T; 0 other;

Query Match 76.7%; Score 13.8; DB 20; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgtctctccaccttggga 18
Db 24 ATGCTCTCCAACCTTAGA 8
||||||| ||| ||

RESULT 11
AAAF69745/C
ID AAF69745 standard; DNA; 23 BP.
XX AC AAF69745;
XX XX 18-APR-2001 (first entry)
XX DE Human IL4Ralpha gene PCR primer #81.
XX KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
XX KW allergic disease; PCR primer; ss.
XX OS Homo sapiens.
XX PI

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PN WO200104270-A1.
XX 18-JAN-2001.
XX PF 13-JUL-2000; 2000WO-US19094.
XX PR 13-JUL-1999; 99US-0143435.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
XX PI Windemuth AK;
XX DR WPI; 2001-103078/11.
XX XX New isolated polynucleotide useful for the identification of
XX PT therapeutics in allergic diseases is new -
XX PS Example 1; Page 63; 188pp; English.
XX CC The present invention relates to polymorphisms of the human interleukin 4
XX CC receptor-alpha gene (IL4R-alpha; see AAF5718 for the reference
XX CC sequence). Polynucleotides comprising polymorphic gene variants are
XX CC useful for therapeutic purposes. For example, where a patient may benefit
XX CC from expression of a particular IL4Ralpha protein isoform, an expression
XX CC vector encoding the isoform may be administered to the patient. It may
XX CC desirable to decrease or block expression of a particular IL4Ralpha
XX CC isogene, which may be done by turning off by transforming a targeted
XX CC organ, tissue or cell population with an expression vector that expresses
XX CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
XX CC identified by these methods may be useful for allergic diseases. The
XX CC present sequence is a PCR primer for human IL4R-alpha.
XX SQ Sequence 23 BP; 10 A; 4 C; 7 G; 2 T; 0 other;

Query Match 74.4%; Score 13.4; DB 22; Length 23;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 catgtctctccacctt 15
Db 16 CATGCTCTCTACCTT 2
||||||| |||||

RESULT 12
AAZ34849
ID AAZ34849 standard; DNA; 20 BP.
XX AC AAZ34849;
XX DT 28-FEB-2000 (first entry)
XX DE Feline CTLA-4 3' PCR primer.
XX KW CTLA-4; feline; cat; recombinant virus; vaccine; immunomodulator;
XX KW tumour; cancer; therapy; PCR; primer; ss.
XX OS Synthetic.
XX OS Felis domesticus.
XX PN WO9957295-A1.
XX PD 11-NOV-1999.
XX PF 30-APR-1999; 99WO-US09504.
XX PR 01-MAY-1998; 98US-0071711.
XX PA (SCHE ) SCHERING-PLOUGH LTD.
XX PA (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX PI Winslow BJ, Cochran MD;

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XX WPI; 2000-062155/05.
DR
XX Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines -
PT
XX
PS Example 1A; Page 73; 230pp; English.
XX
CC This oligonucleotide represents a 3' primer used in a nested-PCR
CC amplification of feline CTLA-4 cDNA (see AA234840). The invention
CC relates to a recombinant virus that contains at least one foreign
CC nucleic acid, inserted into a nonessential genomic region, that
CC encodes feline CD80, CD86 or CTLA-4 protein, or their
CC immunogenic fragments, and is expressed when the recombinant
CC virus is introduced into a suitable host. The recombinant virus
CC may further comprise a foreign nucleic acid encoding an immunogen
CC derived from a feline pathogen. It is used to enhance or suppress
CC an immune response in a feline, particularly as a vaccine.
XX
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match 73.3%; Score 13.2; DB 21; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtcctccaccttga 18
Db |||| |||||||||
2 catgagctccaccttga 19

RESULT 13
AAZ34797
ID AA234797 standard; DNA; 20 BP.
XX
AC AA234797;
XX
DT 15-FEB-2000 (first entry)
XX
DE Cat CTLA-4 receptor cDNA 3' PCR primer.
XX
KW CTLA-4; CD152; receptor; cat; vaccine; PCR; primer; ss.
XX
OS Synthetic.
XX
OS Felis domesticus.
XX
PN WO9957271-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09502.
XX
PR 01-MAY-1998; 98US-0071699.
XX
PA (TEXA ) TEXAS A & M SYSTEM.
XX
PI Collison EW, Hash SM, Choi I;
XX
DR WPI; 2000-052972/04.
XX
PT Novel feline proteins used to produce feline vaccines which prevent
PT infectious disease or to promote growth in homologous or heterologous
PT species -
XX
PS Example 1A; Page 38; 186pp; English.
XX
CC This oligonucleotide represents a 3' primer used in nested PCR
CC amplification of feline CTLA-4 (CD152) receptor 5' region cDNA (see
CC AA234787). The template was the product of a first PCR amplification
CC of peripheral blood mononuclear cell cDNA. The invention provides
CC nucleic acids encoding feline CD80 ligand, feline CD86 (B7-2)
CC ligand, feline CD28 receptor or feline CTLA-4 receptor, as well as
CC vectors comprising the nucleic acids, and polypeptides encoded by

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CC the nucleic acids. It also provides vaccines comprising the CD80,
CC CD86, CD28 or CTLA-4 polypeptides and further comprising immunogens
CC derived from pathogens, as well as vaccines capable of enhancing an
CC immune response and vaccines capable of suppressing an immune
CC response.
XX
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;

Query Match 73.3%; Score 13.2; DB 21; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtcctccaccttga 18
Db |||| |||||||||
2 catgagctccaccttga 19

RESULT 14
AAH19003
ID AAH19003 standard; DNA; 24 BP.
XX
AC AAH19003;
XX
DT 21-JUN-2001 (first entry)
XX
DE Reverse primer used to amplify UCP3 gene promoter region 1.
XX
KW UCP3; uncoupling protein 3; polymorphism; obesity;
XX
KW diabetes mellitus; ss.
XX
OS Homo sapiens.
XX
PN WO200118232-A2.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US24784.
XX
PR 08-SEP-1999; 99US-0152789.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PA (STEP/) STEPHENS J C.
XX
PI Chew A, Choi JY, Denton RR, Nandabalan K;
XX
DR WPI; 2001-218562/22.
XX
PT Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
PT useful for the design of drugs for treating obesity -
XX
PS Example 1; Page 33; 94pp; English.
XX
CC The present invention relates to the human uncoupling protein 3
CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms.
CC The polymorphisms are associated with obesity, especially
CC diabetes mellitus associated obesity. They polymorphisms may be
CC identified and analysed to determine whether an individual is
CC susceptible to obesity and may be used as the basis for targeted
CC design of drugs to treat obesity. The present sequence was used in
CC the identification and amplification of UCP3 polymorphisms.
XX
SQ Sequence 24 BP; 2 A; 9 C; 4 G; 9 T; 0 other;

Query Match 73.3%; Score 13.2; DB 22; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catgtcctccaccttga 18
Db |||||| |||||||
5 cctgtcctctcttcttga 22

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RESULT 15
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ID AAH19025 standard; DNA; 24 BP.
XX
AC AAH19025;
XX
DT 21-JUN-2001 (first entry)
XX
DE Reverse primer used to sequence UCP3 gene promoter region 1.
XX
KW UCP3; uncoupling protein 3; polymorphism; obesity;
KW diabetes mellitus; ss.
XX
OS Homo sapiens.
XX
PN WO200118232-A2.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-US24784.
XX
PR 08-SEP-1999; 99US-0152789.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (STEP/) STEPHENS J C.
XX
PI Chew A, Choi JY, Denton RR, Nandabalan K;
XX
DR WPI; 2001-218562/22.
XX
XX
XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
PT useful for the design of drugs for treating obesity -
XX
XX Example 1; Page 35; 94pp; English.
XX
XX The present invention relates to the human uncoupling protein 3
CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms.
CC The polymorphisms are associated with obesity, especially
CC diabetes mellitus associated obesity. They polymorphisms may be
CC identified and analysed to determine whether an individual is
CC susceptible to obesity and may be used as the basis for targeted
CC design of drugs to treat obesity. The present sequence was used in
CC the identification and amplification of UCP3 polymorphisms.
XX
SQ Sequence 24 BP; 2 A; 9 C; 4 G; 9 T; 0 other;
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Query Match 73.3%; Score 13.2; DB 22; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catgtctctccaccttgga 18
| | | | | | | | | |
Db 5 cctgtctctctcttgga 22

Search completed: October 12, 2002, 17:08:04
Job time: 9749 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:37 ; Search time 191.26 Seconds
(without alignments)
23.117 Million cell updates/sec

Title: US-09-945-131-6

Perfect score: 18

Sequence: 1 catgtcctccacccttggga 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCRUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	18	100.0	18	5	PCT-US92-00626-2
3	14.8	82.2	30	2	US-08-465-971B-5
4	14.8	82.2	30	2	US-08-465-971B-9
5	14.8	82.2	34	2	US-08-465-971B-7
6	13.8	76.7	41	1	US-08-675-153-5
7	13.8	76.7	41	2	US-08-841-252-5
8	13.8	76.7	41	2	US-08-881-571-5
9	13.2	73.3	30	3	US-09-130-663-9
10	13.2	73.3	30	3	US-09-432-335-9
11	13.2	73.3	33	1	US-08-505-058-12
12	13.2	73.3	33	1	US-08-505-058-12
13	13.2	73.3	50	4	US-09-455-679-16
14	13.2	73.3	50	4	US-09-455-679-17
15	12.8	71.1	25	3	US-09-255-912-4
16	12.8	71.1	28	2	US-08-859-998-888
17	12.8	71.1	28	4	US-09-225-928-888
18	12.8	71.1	37	5	PCT-US93-11638-6
19	12.4	68.9	18	4	US-09-177-359-15
20	12.4	68.9	23	3	US-08-891-789B-27
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22	12.4	68.9	45	2	US-08-495-695B-25
23	12.4	68.9	45	2	US-08-495-695B-25
24	12.4	68.9	45	5	PCT-US94-14436-25
25	12.4	68.9	45	5	PCT-US94-14436-26
26	12.4	68.9	50	1	US-08-207-901-34
27	12.2	67.8	25	4	US-08-702-665A-11

Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 180, App
Sequence 180, App
Sequence 20, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 77, Appl
Sequence 18, Appl
Sequence 48, Appl
Sequence 53, Appl
Sequence 9, Appl
Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-369-282-2
; Sequence 2, Application US/08369282
; Patent No. 5593974
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, ROBERT D
; APPLICANT: SIMONS, MICHAEL
; APPLICANT: EDELMAN, ELAZER
; APPLICANT: LANGER, ROBERT S
; APPLICANT: DEKEYSER, JEAN-LUC
; TITLE OF INVENTION: LOCALIZED OLIGONUCLEOTIDE THERAPY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,282
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/855,416
; FILING DATE:
; APPLICATION NUMBER: US 792,146
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 723,454
; FILING DATE: 28-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MIT5583CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /standard_name= "ANTISENSE HUMAN
; OTHER INFORMATION: NMHC"
; OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO HUMAN NMHC"
US-08-369-282-2

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Best Local Similarity 100.0%; Pred. No. 3.1;
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DB 1 CATGTCTCCACCTTGGGA 18

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; Sequence 2, Application PC/TUS9200626
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, ROBERT D
; APPLICANT: SIMONS, MICHAEL
; APPLICANT: EDELMAN, ELAZER
; APPLICANT: LANGER, ROBERT S
; APPLICANT: DEKEYSER, JEAN-LUC
; TITLE OF INVENTION: LOCALIZED OLIGONUCLEOTIDE THERAPY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US92/00626
; FILING DATE: 19921105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 792,146
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 723,454
; FILING DATE: 28-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MIT5583CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /standard_name= "ANTISENSE HUMAN
; OTHER INFORMATION: NMHC"
; OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO HUMAN NMHC"

PCT-US92-00626-2

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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgtcctccaccttggga 18
|||||
DB 1 CATGTCTCCACCTTGGGA 18

RESULT 3
US-08-465-971B-5
; Sequence 5, Application US/08465971B
; Patent No. 5942414
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,971B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-465-971B-5

Query Match 82.2%; Score 14.8; DB 2; Length 30;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catgtcctccaccttggga 18
|||||
DB 12 CATGAACCTCCACCTTGGGA 29

RESULT 4
US-08-465-971B-9
; Sequence 9, Application US/08465971B
; Patent No. 5942414
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.971B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-465-971B-9

Query Match 82.2%; Score 14.8; DB 2; Length 30;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccacccttggg 18
||||| ||||| ||||| |||||
Db 12 CATGAACCTCCACCTTGA 29

RESULT 5
US-08-465-971B-7
; Sequence 7, Application US/08465971B
; Patent No. 5942414
; GENERAL INFORMATION:
; APPLICANT: Yi Li and Mark D. Adams
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: US
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465.971B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-465-971B-7

Query Match 82.2%; Score 14.8; DB 2; Length 34;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccacccttggg 18
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Db 16 CATGAACCTCCACCTTGA 33

RESULT 6
US-08-675-153-5/c
; Sequence 5, Application US/08675153
; Patent No. 5677124
; GENERAL INFORMATION:
; APPLICANT: DuBois, Dwight
; APPLICANT: Winkler, Matthew
; APPLICANT: Pasloske, Brittan L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
; TITLE OF INVENTION: RNA STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675.153
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-675-153-5

Query Match 76.7%; Score 13.8; DB 1; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atgtctccacccttggg 18
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RESULT 7
US-08-841-252-5/c

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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/881,571
; FILING DATE: Concurrently Herewith
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-571-5

Query Match 76.7%; Score 13.8; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 3,1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels

QY 2 atgtctctccaccttggga 18
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Db 24 ATGTCTCTCCAACCTTAGA 8

RESULT 9
US-09-282-054-5/c
; Sequence 5, Application US/09282054
; Patent No. 6214982
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; NUMBER OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,054
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,571
; FILING DATE:
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; PRIOR APPLICATION DATA:

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; EARLIER FILING DATE: 1997-08-06

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; OTHER INFORMATION: Primer
US-09-455-679-17

Query Match      73.3%; Score 13.2; DB 4; Length 50;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 26 cagtcgcgcaccttga 43

RESULT 15
US-09-255-912-4
; Sequence 4, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-255-912-4

Query Match      71.1%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catgtctccaccttg 16
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Db 1 catgtctccaccttg 16

Search completed: October 12, 2002, 16:54:38
Job time: 8993 sec
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US-09-455-679-16
; Sequence 16, Application US/09455679
; Patent No. 6329186
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Svendsen, Allan
; APPLICANT: Bojsen, Kirsten
; APPLICANT: Vind, Jesper
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Glucoamylases With N-Terminal Extensions
; FILE REFERENCE: 5691.200-US
; CURRENT APPLICATION NUMBER: US/09/455,679
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: PA 1998 01616
; EARLIER FILING DATE: 1998-12-07
; EARLIER APPLICATION NUMBER: PA 1999 00409
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/111,674
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/126,740
; EARLIER FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-455-679-16

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Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 26 cagtcgcgcaccttga 43

RESULT 14
US-09-455-679-17
; Sequence 17, Application US/09455679
; Patent No. 6329186
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Svendsen, Allan
; APPLICANT: Bojsen, Kirsten
; APPLICANT: Vind, Jesper
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Glucoamylases With N-Terminal Extensions
; FILE REFERENCE: 5691.200-US
; CURRENT APPLICATION NUMBER: US/09/455,679
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: PA 1998 01616
; EARLIER FILING DATE: 1998-12-07
; EARLIER APPLICATION NUMBER: PA 1999 00409
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/111,674
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/126,740
; EARLIER FILING DATE: 1999-03-29
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 50
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; ORGANISM: Artificial Sequence
; FEATURE:
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:51:19 ; Search time 2530.15 Seconds
(without alignments)
148.876 Million cell updates/sec

Title: US-09-945-131-7

Perfect score: 18
Sequence: 1 gatcaggcgtgcctcaaa 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: gb_un: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	18	100.0	18	6	A47180	A47180 Sequence 23
4	18	100.0	18	6	AR034514	AR034514 Sequence
c 5	18	100.0	18	6	AR034516	AR034516 Sequence
c 6	18	100.0	18	6	AR034535	AR034535 Sequence
7	18	100.0	18	6	AR034536	AR034536 Sequence
8	18	100.0	18	6	AR048614	AR048614 Sequence
c 9	18	100.0	18	6	AR048616	AR048616 Sequence
c 10	18	100.0	18	6	AR048635	AR048635 Sequence
11	18	100.0	18	6	AR048636	AR048636 Sequence
12	18	100.0	18	6	AX081383	AX081383 Sequence
13	18	100.0	18	6	AX283213	AX283213 Sequence
14	18	100.0	18	6	AX283283	AX283283 Sequence
15	18	100.0	18	6	I33927	I33927 Sequence 5
16	18	100.0	18	6	I43417	I43417 Sequence 22
c 17	18	100.0	18	6	I43419	I43419 Sequence 24
18	18	100.0	18	6	I62694	I62694 Sequence 2
c 19	18	100.0	27	6	AR009814	AR009814 Sequence
c 20	15	83.3	30	6	I43416	I43416 Sequence 21
c 21	13.4	74.4	30	6	AR034512	AR034512 Sequence
c 22	13.4	74.4	30	6	AR048612	AR048612 Sequence
23	13.4	74.4	37	6	AX179598	AX179598 Sequence
24	13.2	73.3	18	6	AR034550	AR034550 Sequence
c 25	13.2	73.3	39	6	AR021477	AR021477 Sequence
c 26	13.2	73.3	39	6	AR061315	AR061315 Sequence
c 27	13.2	73.3	39	6	AR100113	AR100113 Sequence
c 28	13.2	73.3	39	6	AR175970	AR175970 Sequence
29	13	72.2	24	6	AX298054	AX298054 Sequence
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c 31	12.8	71.1	46	6	AR082248	AR082248 Sequence
c 32	12.8	71.1	46	6	AR082271	AR082271 Sequence
c 33	12.8	71.1	46	6	AR120790	AR120790 Sequence
c 34	12.8	71.1	46	6	AR120813	AR120813 Sequence
c 35	12.8	71.1	46	6	I78294	I78294 Sequence 92
c 36	12.8	71.1	46	6	I78317	I78317 Sequence 11
c 37	12.4	68.9	38	6	AR119237	AR119237 Sequence
c 38	12.4	68.9	39	6	AR119238	AR119238 Sequence
c 39	12.4	68.9	39	6	AX031333	AX031333 Sequence
c 40	12.2	67.8	18	6	AR009808	AR009808 Sequence
c 41	12.2	67.8	20	6	AR009488	AR009488 Sequence
c 42	12.2	67.8	20	6	AR064146	AR064146 Sequence
c 43	12.2	67.8	20	6	AX296440	AX296440 Sequence
c 44	12.2	67.8	20	6	I35567	I35567 Sequence 14
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ALIGNMENTS

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DEFINITION		A42368					
ACCESSION		A42368.1	GI:2297844				
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							
FEATURES							
source							

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Best Local Similarity	100.0%; Pred. No. 1.6e+02;	Best Local Similarity	100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db 1 GATCAGCGTGCCTCAAA 18		Db 1 GATCAGCGTGCCTCAAA 18	
RESULT 2		RESULT 4	
A44393		AR034514	
LOCUS	18 bp DNA linear PAT 07-MAR-1997	LOCUS	18 bp DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 23 from Patent EP0653439.	DEFINITION	Sequence 17 from patent US 5869462.
ACCESSION	A44393	ACCESSION	AR034514
VERSION	A44393.1 GI:2299222	VERSION	AR034514.1 GI:5950119
KEYWORDS	human.	KEYWORDS	Unknown.
SOURCE	human.	SOURCE	Unknown.
ORGANISM	Homo sapiens	ORGANISM	Unknown.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE	1 (bases 1 to 18)
AUTHORS	Peyman,A.D., Uhlmann,E.D., Mag,M., Kretzschmar,G.D., Helsenberg,M.D. and Winkler,I.D.	AUTHORS	Dzau,V.J.
TITLE	Stabilized oligonucleotids and the use thereof	TITLE	Inhibition of proliferation of vascular smooth muscle cell
JOURNAL	HOECHST AG (DE)	JOURNAL	Patent: US 5869462-A 17 09-FEB-1999;
COMMENT	Other publication JP 7194385 950801 Other publication CA 2135591 950513 Other publication AU 7779994 950518 Other publication DE 4338704 950518.	FEATURES	Location/Qualifiers 1..18 /organism="unknown" 5 a 5 c 5 g 3 t
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		ORIGIN	
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ORIGIN		Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Best Local Similarity	100.0%; Pred. No. 1.6e+02;		
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		RESULT 5	
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		DEFINITION	Sequence 19 from patent US 5869462.
RESULT 3		ACCESSION	AR034516
A47180		VERSION	AR034516.1 GI:5950121
LOCUS	A47180 18 bp DNA linear PAT 07-MAR-1997	KEYWORDS	Unknown.
DEFINITION	Sequence 23 from Patent EP0680969.	SOURCE	Unknown.
ACCESSION	A47180	ORGANISM	Unknown.
VERSION	A47180.1 GI:2301222	REFERENCE	1 (bases 1 to 18)
KEYWORDS	human.	AUTHORS	Dzau,V.J.
SOURCE	human.	TITLE	Inhibition of proliferation of vascular smooth muscle cell
ORGANISM	Homo sapiens	JOURNAL	Patent: US 5869462-A 19 09-FEB-1999;
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	FEATURES	Location/Qualifiers 1..18 /organism="unknown" 3 a 5 c 5 g 5 t
AUTHORS	Seela,F.P. and Lampe,S.D.	BASE COUNT	
TITLE	Modified oligonucleotides, their preparation and their use	ORIGIN	
JOURNAL	Patent: EP 0680969-A 23 08-NOV-1995;		
	HOECHST AG (DE)		

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
AR034535/c
LOCUS AR034535 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 38 from patent US 5869462.
ACCESSION AR034535
VERSION AR034535.1 GI:5950140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5869462-A 38 09-FEB-1999;
FEATURES Location/Qualifiers
source 1. .18
BASE COUNT 3 a 5 c 5 g 5 t
ORIGIN

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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LOCUS AR034536 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 39 from patent US 5869462.
ACCESSION AR034536
VERSION AR034536.1 GI:5950141
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5869462-A 39 09-FEB-1999;
FEATURES Location/Qualifiers
source 1. .18
BASE COUNT 5 a 5 c 5 g 3 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GATCAGGCGTGCCTCAAA 18

RESULT 8
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LOCUS AR048614 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5821234.

AR048614
ACCESSION AR048614.1 GI:5970957
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5821234-A 17 13-OCT-1998;
FEATURES Location/Qualifiers
source 1. .18
BASE COUNT 5 a 5 c 5 g 3 t
ORIGIN

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GATCAGGCGTGCCTCAAA 18

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LOCUS AR048616 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5821234.
ACCESSION AR048616
VERSION AR048616.1 GI:5970959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5821234-A 19 13-OCT-1998;
FEATURES Location/Qualifiers
source 1. .18
BASE COUNT 3 a 5 c 5 g 5 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 10
AR048635/c
LOCUS AR048635 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 38 from patent US 5821234.
ACCESSION AR048635
VERSION AR048635.1 GI:5970978
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Dzau, V. J.
TITLE Inhibition of proliferation of vascular smooth muscle cell
JOURNAL Patent: US 5821234-A 38 13-OCT-1998;
FEATURES Location/Qualifiers
source 1. .18
BASE COUNT 3 a 5 c 5 g 5 t
ORIGIN


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LOCUS I33927 18 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5593974.
ACCESSION I33927
VERSION I33927.1 GI:1824718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Rosenberg,R.D., Simons,M., Edelman,E., Langer,R.S. and
DeKeyser,J.-L.
TITLE Localized oligonucleotide therapy
JOURNAL Patent: US 5593974-A 5 14-JAN-1997;
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ORIGIN
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Search completed: October 12, 2002, 16:51:20
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 17:08:04 ; Search time 792.17 seconds
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39.012 Million cell updates/sec

Title: US-09-945-131-7

Perfect score: 18

Sequence: 1 gatcaggcgctgctcaaa 18

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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	18	100.0	18	17	AAT37345
9	18	100.0	18	17	AAT51718

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12	18	100.0	18	22	AAF60953	Anti-PCNA oligonuc
13	18	100.0	18	22	AAH49236	Anti-PCNA (prolif
14	18	100.0	18	24	ABL01645	PCNA targeted anti
15	18	100.0	27	14	AAQ37751	PCNA mRNA anti-sen
16	15	83.3	30	16	AAT05427	Rat PCNA mRNA frag
17	13.4	74.4	30	16	AAQ75055	Rat proliferating
18	13.4	74.4	37	22	AAQ09734	Human ZCYTO18 cDNA
19	13.2	73.3	18	17	AAT37348	3 bp mismatch olig
20	13.2	73.3	34	19	AAV36244	PCR primer used to
21	13.2	73.3	39	19	AAV42360	Agouti locus where
22	13.2	73.3	39	20	AAV81347	Mouse agouti mutat
23	13.2	73.3	39	21	AAE62334	3' deletion breakp
24	13.2	73.3	39	24	AAE17270	Intron-exon struct
25	13	72.2	24	24	AAE19121	Rat c-myc mRNA ant
26	12.8	71.1	27	19	AAV26324	Human prostate can
27	12.8	71.1	27	20	AAZ26071	Prostate disease m
28	12.8	71.1	27	21	AAZ87557	Primer specific fo
29	12.8	71.1	27	22	AAO3974	Blomarker UC band
30	12.8	71.1	46	16	AAQ83065	HIV hammerhead mot
31	12.8	71.1	46	16	AAQ83042	HIV hammerhead mot
32	12.4	68.9	38	20	AAZ25748	Reactive oligonuc
33	12.4	68.9	38	20	AAZ21594	Template oligo #2.
34	12.4	68.9	38	20	AAZ21590	Template oligonuc
35	12.4	68.9	38	20	AAZ16068	Template oligonuc
36	12.4	68.9	39	18	AAZ8531	Oligonucleotide DM
37	12.4	68.9	39	20	AAZ84376	Oligonucleotide us
38	12.4	68.9	39	20	AAZ25749	Reactive oligonuc
39	12.4	68.9	39	20	AAZ21595	Template oligo #2
40	12.4	68.9	39	20	AAZ21591	Template oligonuc
41	12.4	68.9	39	20	AAZ16069	Template oligonuc
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43	12.2	67.8	18	19	AAV30104	Antisense oligonuc
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ALIGNMENTS

RESULT 1

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XX AAQ42221;

XX 02-SEP-1993 (first entry)

XX Antisense sequence to PCNA.

XX Antisense; oligonucleotide; inhibit; translation; transcription;

XX target; nucleic acid; mammal; tissue; hybridise; combine; carrier;

XX polyethylene oxide; polypropylene oxide; copolymer; ss.

XX Synthetic.

XX WO9308845-A.

XX 13-MAY-1993.

XX 05-NOV-1992; 92WO-US09626.

XX 08-NOV-1991; 91US-0792146.

XX 18-MAR-1992; 92US-0855416.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Dekeyser J, Edelman E, Langer RS, Rosenberg RD;

XX Simons M;

XX WPI; 1993-167406/20.

PT Inhibiting translation or transcription of target nucleic acid -
PT by local administration in vivo of oligo:nucleotide complementary
to target sequence
XX
PS Disclosure; Page 41; 65pp; English.
XX
CC The sequences given in AAQ42217-21 are antisense oligonucleotides
CC which were used to inhibit translation or transcription of target
CC nucleic acids at a locus in vivo. The oligonucleotide are applied
CC directly to a tissue at the locus within the body of a mammal and
CC they are able to penetrate the cells of the tissue, hybridise/combine
CC with the target nucleic acid inhibiting intracellular translation or
CC transcription. The oligonucleotide are incorporated into a carrier
XX eg. a polyethylene oxide-polypropylene oxide copolymer.
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gatcaggcgtgcctcaaa 18
|||||
DB 1 gatcaggcgtgcctcaaa 18

RESULT 2
AAQ35160
ID AAQ35160 standard; DNA; 18 BP.
AC
AC AAQ35160;
XX
XX 02-JUN-1993 (first entry)
XX
XX PCNA antisense oligonucleotide.
XX
XX Antisense; inhibit; protein coding genes; regulatory DNA; stroke;
XX endonuclease; vascular restenosis; myocardial infarction; embolism;
XX peripheral muscular disease; peripheral angioplasty; thrombophlebitis;
XX vasculitis; angina; Budd-Chiari syndrome; thrombosis; atherosclerosis;
XX hypertension; primary pulmonary; proliferative glomerulonephritis;
XX acute respiratory distress syndrome; idiopathic pulmonary fibrosis;
XX emphysema; ss.
XX
XX Synthetic.
XX
XX WO9301286-A.
XX
XX 21-JAN-1993.
XX
XX 23-JUN-1992; 92WO-US05305.
XX
XX 28-JUN-1991; 91US-0723454.
XX
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Dekeyser J, Edelman E, Langer RS, Rosenberg RD;
XX Simons M,
XX WPI; 1993-045491/05.
XX
XX Localised therapy using anti-sense oligo:nucleotide(s) - which
XX penetrate through tissue cell to hybridise with target m-RNA and
XX inhibit expression of the gene, for treatment of vascular
XX disorders, atherosclerosis, hypertension, etc.
XX
XX Example 4; Page 33; 59pp; English.
XX
XX The sequences given in AAQ34766-67 and AAQ35258-60 are antisense
XX oligonucleotides which were used in a method of inhibiting a target
XX nucleic acid sequence. The method may be used for inhibiting the
XX expression of protein coding genes as well as regulatory DNA.

CC Application of the antisense oligonucleotides to a defined locus in
CC vivo allows their use when systemic administration is not possible,
CC ie. systemically administered oligos may be rendered inefficient by
CC endonucleases before they reach their targets. This method may be
CC used in the treatment of vascular disorders, particularly vascular
CC restenosis, myocardial infarction, peripheral muscular disease.
CC peripheral angioplasty, thrombophlebitis, stroke, embolism,
CC vasculitis, angina, Budd-Chiari syndrome, thrombosis, atherosclerosis,
CC hypertension, primary pulmonary hypertension, proliferative glomerulo-
CC nephritis, acute respiratory distress syndrome, idiopathic pulmonary
CC fibrosis or emphysema.
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gatcaggcgtgcctcaaa 18
|||||
DB 1 gatcaggcgtgcctcaaa 18

RESULT 3
AAT44447
ID AAT44447 standard; DNA; 18 BP.
XX
XX AAT44447;
XX
XX 27-JAN-1997 (first entry)
XX
XX Antisense oligonucleotide against PCNA gene.
XX
XX 8-azapurine; modification; stronger complex; inhibition;
XX proliferating cell nuclear antigen; ss.
XX
XX Synthetic.
XX
XX EP680969-A2.
XX
XX 08-NOV-1995.
XX
XX 26-APR-1995; 95EP-0106230.
XX
XX 02-MAY-1994; 94DE-4415370.
XX
XX (FARH) HOECHST AG.
XX
XX Lampe S, Seela F;
XX WPI; 1995-375165/49.
XX
XX New oligo:nucleotide(s) contg. 8-aza:purine base - useful as
XX therapeutic and diagnostic agents with more stable hybridisation to
XX target nucleic acid
XX
XX Disclosure; Page 43; 51pp; German.
XX
XX AAT44425-54 are antisense oligonucleotides which have at least one
XX 8-azapurine base. The presence of an 8-azapurine base results in
XX significantly stronger complexing when hybridising to target nucleic
XX acids. The present sequence is against proliferating cell nuclear
XX antigen (PCNA) gene.
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
XX
Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gatcaggcgtgcctcaaa 18

PT kinase genes, partic. for preventing restenosis after
PT cardiovascular angioplasty.

XX
PS Disclosure; Page 13; 77pp;

AAQ75079 is a rat proliferative cell nuclear antigen (PCNA) antisense oligomer, which inhibits the expression of PCNA. When administered to a site of lesion formation the antisense oligomer helps prevent restenosis, after cardiovascular angioplasty.

Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;
XX
SQ

```
Query Match      100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 gatcaggcgtgcctcaa 18
|||||
Db 1 gatcaggcgtgcctcaa 18

RESULT 7

AAQ88735
ID AAQ88735 standard; DNA: 18 BP.

XX
AC

XX
DT 27-FEB-1996 (first entry)

XX Human PCNA modified antisense oligonucleotide. DE

XX antisense; analogue; non-terminal pyrimidine; phosphorothioate;
KW backbone; treatment; HIV; human immunodeficiency virus; HSV;
KW herpes simplex virus; cancer; integrin; cell adhesion receptor;
KW infection; diagnosis; nuclease resistance; ss.
KW

XX Homo sapiens.
OS

XX
PN EP653439-A2.

XX 17-MAY-1995.
PD

XX 07-NOV-1994: 94EP-0117513.

12-NOV-1993: 93DE-4338704

PA (FARH) HOECHST AG-

XX
PI
PI
PI

XX
DR WPI; 1995-180677/24.

XX New anti:sense oligo:nucleotide analogues - with modified
PT non-terminal pyrimidine nucleotide units, useful for treating viral
PT infections, cancer, etc.

XX
PS
Claim 1: page 29: 36pp: German.

The antisense oligonucleotide (ON) shown is a derivative of an equivalent wild type Human proliferating cell nuclear antigen ON, in which at least one, esp. 2-10, non-terminal pyrimidine nucleotide(s) is/are modified. The modification may be: (a) replacement of a phosphodiester linkage by: a phosphorothioate (PS), -dithioate, -aramidate; borano-, alkyl-, aralkyl-phosphate; 2,2',2'-trichloro-1,1-dimethyl-, alkyl- or aryl- phosphonate linkage; or (3'-thio)formacetal-, methylhydroxylamine, oxime, methylenedimethylhydrazo, dimethylene sulphone or silyl linkage; (b) replacement of a sugar phosphate backbone by a 'morpholinonucleoside' oligomer; (c) replacement of beta-D-2-deoxyribose by another sugar or carbocyclic, open-chain or bicyclic sugar analogue; or (d) replacement of the natural nucleoside base by an analogue, e.g. 5-hydroxymethyl-uridine. The 5' and/or 3' terminus may also be modified

```

Db      1 gatcaggcgtgcctcaaa 18
|||||
RESULT 9
AAT51718
ID      AAT51718 standard; DNA; 18 BP.
XX
AC      AAT51718;
XX
XX      09-APR-1997 (first entry)
DT
DE
DE      Oligonucleotide 2342.
XX
KW      Antisense oligonucleotide; rat; cdc gene; lipid complex; restenosis;
KW      aminomannose derivatised cholesterol; vascular smooth muscle; liposome;
KW      cell-cycle regulatory gene; proliferating cell nuclear antigen; PTCA;
KW      inhibitor; neointima hyperplasia; angioplasty injury; PCNA;
KW      percutaneous transluminal coronary angioplasty; ss.
XX
OS      Synthetic.
XX
PN      WO9624333-A1.
XX
PD      15-AUG-1996.
XX
PF      09-FEB-1996; 96WO-US01807.
XX
PR      10-FEB-1995; 95US-0386579.
XX
PA      (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI      Male-Brunne R;
XX
DR      WPI; 1996-384195/38.
XX
PT      Vascular targeting of therapeutic or imaging agents - using
PT      liposome(s) contg. amino:mannose-derivatised cholesterol
XX
PS      Example 2; Page 17; 45pp; English.
XX
CC      This sequence represents an antisense oligonucleotide that targets the
CC      rat proliferating cell nuclear antigen (PCNA) gene. This sequence is
CC      complexed with a lipid to form a lipid construct of the invention. The
CC      lipid constructs of the invention also contain an aminomannose
CC      derivatised cholesterol, such as derivatised
CC      dioleoylphosphatidylethanolamine (DOPE). The aminomannose used is
CC      preferably 6-(cholest-5-en-3beta-yloxy)hexyl 6-amino-6-deoxy-1-thiol-
CC      alpha-D-mannopyranosidase. The lipid constructs are used to target a
CC      therapeutic or imaging agent to vascular smooth muscle. By including
CC      the derivatised cholesterol in the lipid component of the liposomes, the
CC      uptake of the liposome by smooth muscle cells is greatly increased.
CC      Administration of two antisense oligonucleotides (such as this sequence
CC      and AAT51718) that block the cell-cycle regulatory genes for PCNA and
CC      cdc2 has previously been shown to inhibit neointima hyperplasia
CC      following angioplasty injury. The liposomes of the invention can be used
CC      for the delivery of an anti-restenosis oligonucleotide (that prevents
CC      neointima formation) during percutaneous transluminal coronary
CC      angioplasty (PTCA).
XX
SQ      Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match      100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 gatcaggcgtgcctcaaa 18
        |||||||
Db      1 gatcaggcgtgcctcaaa 18

RESULT 10
AAT51718
ID      AAT51718 standard; DNA; 18 BP.
XX
AC      AAT51718;
XX
XX      09-APR-1997 (first entry)
DT
DE
DE      Oligonucleotide 2342.
XX
KW      Antisense oligonucleotide; rat; cdc gene; lipid complex; restenosis;
KW      aminomannose derivatised cholesterol; vascular smooth muscle; liposome;
KW      cell-cycle regulatory gene; proliferating cell nuclear antigen; PTCA;
KW      inhibitor; neointima hyperplasia; angioplasty injury; PCNA;
KW      percutaneous transluminal coronary angioplasty; ss.
XX
OS      Synthetic.
XX
PN      WO9624333-A1.
XX
PD      15-AUG-1996.
XX
PF      09-FEB-1996; 96WO-US01807.
XX
PR      10-FEB-1995; 95US-0386579.
XX
PA      (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI      Male-Brunne R;
XX
DR      WPI; 1996-384195/38.
XX
PT      Vascular targeting of therapeutic or imaging agents - using
PT      liposome(s) contg. amino:mannose-derivatised cholesterol
XX
PS      Example 2; Page 17; 45pp; English.
XX
CC      This sequence represents an antisense oligonucleotide that targets the
CC      rat proliferating cell nuclear antigen (PCNA) gene. This sequence is
CC      complexed with a lipid to form a lipid construct of the invention. The
CC      lipid constructs of the invention also contain an aminomannose
CC      derivatised cholesterol, such as derivatised
CC      dioleoylphosphatidylethanolamine (DOPE). The aminomannose used is
CC      preferably 6-(cholest-5-en-3beta-yloxy)hexyl 6-amino-6-deoxy-1-thiol-
CC      alpha-D-mannopyranosidase. The lipid constructs are used to target a
CC      therapeutic or imaging agent to vascular smooth muscle. By including
CC      the derivatised cholesterol in the lipid component of the liposomes, the
CC      uptake of the liposome by smooth muscle cells is greatly increased.
CC      Administration of two antisense oligonucleotides (such as this sequence
CC      and AAT51718) that block the cell-cycle regulatory genes for PCNA and
CC      cdc2 has previously been shown to inhibit neointima hyperplasia
CC      following angioplasty injury. The liposomes of the invention can be used
CC      for the delivery of an anti-restenosis oligonucleotide (that prevents
CC      neointima formation) during percutaneous transluminal coronary
CC      angioplasty (PTCA).
XX
SQ      Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match      100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 gatcaggcgtgcctcaaa 18
        |||||||
Db      1 gatcaggcgtgcctcaaa 18

RESULT 11
AAAL3833
ID      AAAL3833 standard; DNA; 18 BP.
XX
AC      AAAL3833;
XX
XX      27-JUL-2000 (first entry)
DT
DE      PCNA phosphorothioate antisense oligonucleotide SEQ ID NO:7.
XX
KW      Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW      PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW      recurrent stenosis; cardiovascular injury; ss.

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```

AAT39739
ID      AAT39739 standard; DNA; 18 BP.
XX
AC      AAT39739;
XX
XX      15-APR-1997 (first entry)
DT
DE      Rat PCNA gene antisense oligonucleotide.
XX
KW      Inhibition; cancer cell; cytoplasm; vascular smooth muscle cell; nuclei;
KW      aminomannose-derivatised cholesterol component; Amch; VSMC; ss.
XX
OS      Synthetic.
XX
PN      WO9624334-A1.
XX
PD      15-AUG-1996.
XX
PF      08-FEB-1996; 96WO-US01960.
XX
PR      10-FEB-1995; 95US-0386577.
XX
PA      (NEXS-) NEXSTAR PHARM INC.
XX
PI      Male-Brunne R, Proffitt R;
XX
DR      WPI; 1996-384196/38.
XX
PT      Novel lipid construct contg. an amino:mannose-derivatised
PT      cholesterol - useful for delivery of therapeutic or imaging agent to
PT      cell cytoplasm, esp. for anti-sense oligo:nucleotide(s) used to
PT      inhibit growth of e.g. cancers
XX
PS      Claim 21; Page 40; 49pp; English.
XX
CC      The sequences given in AAT39738-39 represent oligonucleotides which
CC      may be used in the method of the invention to inhibit the growth of
CC      vascular smooth muscle cells. The oligonucleotides are administered
CC      to the cytoplasm of a cell by administration of a lipid construct that
CC      includes an aminomannose-derivatised cholesterol component. The
CC      aminomannose-derivatised component is pref. 6-(cholest-5-en-3beta-
CC      yloxy)hexyl-6-amino-6-deoxy-1-thio-alpha-D-mannopyranoside (Amch).
CC      The use of a derivatised cholesterol component provides targeting
CC      to vascular smooth muscle cells without the use of viral material
CC      and the lipid construct allows more efficient delivery of
CC      oligonucleotides to the cytoplasm and nuclei than known constructs.
CC      The oligonucleotides can be used to inhibit the growth of cancer cells.
XX
SQ      Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match      100.0%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 gatcaggcgtgcctcaaa 18
        |||||||
Db      1 gatcaggcgtgcctcaaa 18

RESULT 11
AAAL3833
ID      AAAL3833 standard; DNA; 18 BP.
XX
AC      AAAL3833;
XX
XX      27-JUL-2000 (first entry)
DT
DE      PCNA phosphorothioate antisense oligonucleotide SEQ ID NO:7.
XX
KW      Murine; mouse; platelet derived growth factor receptor beta; vasotropic;
KW      PDGFR-beta; phosphorothioate; antisense oligonucleotide; restenosis;
KW      recurrent stenosis; cardiovascular injury; ss.

```

```

XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "phosphorothioate linkages"
XX
XX CA2228977-A1.
XX PN
XX XX
XX PD
XX PF
XX PF 03-FEB-1998; 98CA-2228977.
XX PR
XX PR 07-NOV-1997; 97CA-2215360.
XX PA (EDEL/) EDELMAN E R.
XX PA (ROSE/) ROSENBERG R D.
XX PA (SIRO/) SIROIS M G.
XX PA (SIMO/) SIMONS M.
XX
XX PI Edelman ER, Rosenberg RD, Sirois MG, Simons M;
XX XX WPI; 2000-283933/25.
XX
XX PT Antisense inhibition of platelet derived growth factor beta-receptor
XX PT subunit expression for the prevention of restenosis -
XX XX
XX PS Claim 27; Page 27; 43pp; English.
XX
XX CC A method has been developed for preventing restenosis following vascular
XX CC injury by antisense inhibition of platelet derived growth factor
XX CC beta-receptor subunit (PDGFR-beta) expression. The method is used for
XX CC the prevention of restenosis (recurrent stenosis (narrowing of a duct or
XX CC canal), especially of a valve in the heart, after surgical correction of
XX CC the primary condition) following cardiovascular injury. The present
XX CC sequence represents a phosphorothioate antisense oligonucleotide for
XX CC PCNA.
XX
XX XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
   |||||
Db 1 gatcaggcgtgcctcaaa 18

RESULT 12
AAAF60953
ID AAFA60953 standard; DNA; 18 BP.
XX
XX AC AAFA60953;
XX
XX XX 15-MAY-2001 (first entry)
XX
XX DE Anti-PCNA oligonucleotide SEQ ID 62.
XX
XX KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
XX KW antiproliferative; antiproliferative; antiproliferative;
XX KW tumor therapy; drug; ss.
XX
XX OS Unidentified.
XX
XX PN DE19935302-A1.
XX
XX PD 08-FEB-2001.
XX
XX PF 28-JUL-1999; 99DE-1035302.
XX

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PR 28-JUL-1999; 99DE-1035302.
XX
XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
XX PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX XX WPI; 2001-203679/21.
XX
XX PT New substituted aryl conjugates of parent molecules, especially
XX PT oligonucleotides, having improved transmembrane and intracellular
XX PT transport properties, useful as medicaments or diagnostic agents -
XX
XX PS Disclosure; Page 8; 28pp; German.
XX
XX CC This invention describes a novel conjugate (I) which consists of (A) a
XX CC molecule to be transported and (B) at least one aryl residue of formula
XX CC -Ar-(X-C(Y)-R1)n (II). Ar = group containing at least one aromatic
XX CC ring; X = O or N (sic); Y = O, S or NH-R2 (sic); R1 = optionally
XX CC substituted 1-23C alkyl (optionally containing double and/or triple
XX CC bonds); R2 = optionally substituted 1-18C alkyl (optionally containing
XX CC double and/or triple bonds); n = integer of 1 or more. (A) is bonded to
XX CC (B) directly or via a chemical group, provided that the chemical group is
XX CC other than CH2-S if the bond is via a phosphodiester linkage of (A). The
XX CC invention also describes (i) the preparation of a conjugate (I') of (A')
XX CC a molecule to be transported and (B') at least one aryl residue (not
XX CC restricted to (II)), by preparing (A') containing a reactive function at
XX CC the position at which (B') is to be bonded, preparing (B') and reacting
XX CC (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded
XX CC via a chemical group) for transporting (A) across biological membranes.
XX CC The products of the invention have cytostatic, virucide, vasotropic,
XX CC dermatological, antiproliferative and antitumor activity and can be used
XX CC for gene therapy. Conjugation of (A) with (B) is useful for transporting
XX CC (A) across biological membranes or into eukaryotic or prokaryotic cells
XX CC (specifically bacterial, yeast or mammalian cells, including human cells,
XX CC particularly tumor cells). Medicaments, diagnostic agents and test kits
XX CC containing (I) are also claimed. Typically (I) are antisense
XX CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
XX CC treating viral infections or diseases associated with integrins or
XX CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);
XX CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
XX CC hybridization. Conjugation with (B) markedly improves the cellular uptake
XX CC of (A), e.g. in tumor cells. (B) include fluorescently labeled, allowing
XX CC in which case the conjugates (I) are fluorescently labeled, allowing
XX CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
XX CC is superior to that obtained using other conjugated groups related to
XX CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
XX CC the scope of (B)) have superior uptake to corresponding fluorescein
XX CC conjugates.
XX
XX XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
   |||||
Db 1 gatcaggcgtgcctcaaa 18

RESULT 13
AAH49236
ID AAH49236 standard; DNA; 18 BP.
XX
XX AC AAH49236;
XX
XX XX 26-NOV-2001 (first entry)
XX
XX DE Anti-PCNA (proliferating cell nuclear antigen) oligonucleotide XXIX.
XX KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
XX KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;

```



```
XX AAQ37751;
XX AC
XX DT
XX DT 17-DEC-2001 (updated)
XX DT 30-JUN-1993 (first entry)
XX PCNA mRNA anti-sense oligonucleotide target sequence.
XX DE Cellular division cycle; cdc; proliferating cell nuclear antigen; ss.
XX KW Non-human.
XX OS
XX PN USN7821415-N.
XX PD 01-JAN-1993.
XX PF 14-JAN-1992; 92US-0821415.
XX PR 14-JAN-1992; 92US-0821415.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX PI Epstein S, Speir E, Unger E;
XX DR WPI; 1993-085860/10.
XX PT Inhibition of re-stenosis of blood vessel - after mechanical
XX PT treatment, to reduce stenosis, using anti-sense oligo:nucleotide(s)
XX PS Disclosure; Page 37; 4lpp; English.
XX CC The sequence is that of a PCNA mRNA target sequence for antisense
XX CC oligonucleotides which may be used for inhibiting translation of
XX CC cellular division cycle (cdc) gene products. They may be used in a
XX CC method of inhibiting restenosis of a mammalian blood vessel after
XX CC mechanical treatment to reduce a stenosis, e.g. coronary balloon
XX CC angioplasty. The sequence spans the AUG translation initiation codon.
XX CC (Note: Revised entry submitted to correct the patent number format of
XX CC US Government-owned NPIS applications to prevent clashes with ongoing US
XX CC granted patent numbers. For further information please visit the Derwent
XX CC web site at www.derwent.com/dwpl/updates/ntis\_us.html.)
XX SQ Sequence 27 BP; 5 A; 9 C; 7 G; 6 U; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcagcgctgcctcaaa 18
   |||||
Db 27 GATCAGCGCTGCCTCAA 10

Search completed: October 12, 2002, 17:08:05
Job time: 9750 sec
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 16:54:38 ; Search time 191.26 Seconds
(without alignments)
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Title: US-09-945-131-7
Perfect score: 18
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c 3	18	100.0	18	1	US-08-241-372-24
4	18	100.0	18	1	US-08-386-579-2
5	18	100.0	18	1	US-08-110-294A-17
c 6	18	100.0	18	1	US-08-110-294A-19
c 7	18	100.0	18	1	US-08-110-294A-38
8	18	100.0	18	1	US-08-110-294A-39
9	18	100.0	18	2	US-08-389-926-17
c 10	18	100.0	18	2	US-08-389-926-19
c 11	18	100.0	18	2	US-08-389-926-38
12	18	100.0	18	2	US-08-389-926-39
13	18	100.0	18	3	US-08-578-686C-28
14	18	100.0	18	3	US-09-094-405-23
15	18	100.0	18	3	US-09-144-112-28
16	18	100.0	18	4	US-08-337-120A-23
17	18	100.0	18	5	PCT-US92-0626-5
c 18	18	100.0	18	5	PCT-US95-05420-22
c 19	18	100.0	18	5	PCT-US95-05420-24
20	18	100.0	18	5	PCT-US96-01807-2
c 21	18	100.0	27	1	US-08-187-785-12
c 22	15	83.3	30	1	US-08-241-372-21
c 23	15	83.3	30	5	PCT-US95-05420-21
c 24	13.4	74.4	30	1	US-08-110-294A-15
c 25	13.4	74.4	30	2	US-08-389-926-15
26	13.2	73.3	18	2	US-08-389-926-53
c 27	13.2	73.3	34	3	US-08-950-860-10

c 28	13.2	73.3	39	1	US-08-465-293A-7	Sequence 7, Appli
c 29	13.2	73.3	39	2	US-08-463-387A-7	Sequence 7, Appli
c 30	13.2	73.3	39	3	US-09-102-977-8	Sequence 8, Appli
c 31	13.2	73.3	39	4	US-09-034-088A-22	Sequence 22, Appl
32	12.8	71.1	27	2	US-08-692-787-57	Sequence 57, Appl
33	12.8	71.1	27	4	US-09-097-193-57	Sequence 92, Appl
c 34	12.8	71.1	46	1	US-08-271-880A-92	Sequence 92, Appl
c 35	12.8	71.1	46	1	US-08-271-880A-115	Sequence 115, App
c 36	12.8	71.1	46	2	US-08-910-408-92	Sequence 92, Appl
c 37	12.8	71.1	46	2	US-08-910-408-115	Sequence 115, App
c 38	12.8	71.1	46	3	US-09-249-213-92	Sequence 92, Appl
c 39	12.8	71.1	46	3	US-09-249-213-115	Sequence 115, App
40	12.4	68.9	38	3	US-09-120-386-3	Sequence 3, Appli
41	12.4	68.9	38	4	US-09-120-501-3	Sequence 3, Appli
c 42	12.4	68.9	39	3	US-09-120-386-4	Sequence 4, Appli
c 43	12.4	68.9	39	4	US-09-120-501-4	Sequence 4, Appli
44	12.2	67.8	18	1	US-08-187-785-6	Sequence 6, Appli
c 45	12.2	67.8	20	1	US-08-116-389-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-369-282-5
; Sequence 5, Application US/08369282
; Patent No. 5593974
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, ROBERT D
; APPLICANT: SIMONS, MICHAEL
; APPLICANT: EDELMAN, ELAZER
; APPLICANT: LANGER, ROBERT S
; APPLICANT: DEKEYSER, JEAN-LDC
; TITLE OF INVENTION: LOCALIZED OLIGONUCLEOTIDE THERAPY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,282
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/855,416
; FILING DATE:
; APPLICATION NUMBER: US 792,146
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 723,454
; FILING DATE: 28-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MIT5583CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna

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; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /standard_name= "ANTISENSE PCNA"
; OTHER INFORMATION: /note= "ANTISENSE SEQUENCE TO PCNA"
US-08-369-282-5

Query Match      100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
   |||||
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 2
US-08-241-372-22
; Sequence 22, Application US/08241372
; Patent No. 5631237
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,372
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-59079-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-241-372-22

Query Match      100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
   |||||
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 3
US-08-241-372-24/c
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; Sequence 24, Application US/08241372
; Patent No. 5631237
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,372
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-59079-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-241-372-24

Query Match      100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
   |||||
Db 1 GATCAGCGTGCCTCAAA 1

RESULT 4
US-08-386-579-2
; Sequence 2, Application US/08386579
; Patent No. 5660855
; GENERAL INFORMATION:
; APPLICANT: M le-Brune, Roxanne
; TITLE OF INVENTION: LIPID CONSTRUCTS FOR TARGETING TO
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vestar, Inc.
; STREET: 650 Cliffside Drive
; CITY: San Dimas
; STATE: California
; COUNTRY: USA
; ZIP: 91773
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/386,579
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cochran, Adam
; REGISTRATION NUMBER: 29,373
; REFERENCE/DOCKET NUMBER: D89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (909)-394-4132
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-386-579-2

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
| | | | | | | | | | | | | | | |
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 5
US-08-110-294A-17
; Sequence 17, Application US/08110294A
; Patent No. 5821234
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-110-294A-19

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
| | | | | | | | | | | | | | | |
Db 18 GATCAGCGTGCCTCAAA 1

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-294A-17

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
| | | | | | | | | | | | | | | |
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 6
US-08-110-294A-19/c
; Sequence 19, Application US/08110294A
; Patent No. 5821234
; GENERAL INFORMATION:
; APPLICANT: Dzaou, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-294A-19

ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,510-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-389-926-17

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGCGGTGCCTCAAA 18

RESULT 10
US-08-389-926-19/c
Sequence 19, Application US/08389926
Patent No. 5869462
GENERAL INFORMATION:
APPLICANT: Dzaou, Victor J
TITLE OF INVENTION: Inhibition of Proliferation of Vascular
NUMBER OF SEQUENCES: 53
TITLE OF INVENTION: Smooth Muscle Cell
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Dr.
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,926
FILING DATE: 16 FEB 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,980
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,510-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-389-926-19

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 1

RESULT 11
US-08-389-926-38/c
Sequence 38, Application US/08389926
Patent No. 5869462
GENERAL INFORMATION:
APPLICANT: Dzaou, Victor J
TITLE OF INVENTION: Inhibition of Proliferation of Vascular
NUMBER OF SEQUENCES: 53
TITLE OF INVENTION: Smooth Muscle Cell
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Dr.
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,926
FILING DATE: 16 FEB 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,980
FILING DATE: 19-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/944,882
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,510-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-389-926-38

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGGTGCCTCAAA 1

RESULT 12
US-08-389-926-39
Sequence 39, Application US/08389926
Patent No. 5869462

;; GENERAL INFORMATION:
;; APPLICANT: Dzau, Victor J
;; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
;; TITLE OF INVENTION: Smooth Muscle Cell
;; NUMBER OF SEQUENCES: 53
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Dr.
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/389,926
;; FILING DATE: 16 FEB 1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/063,980
;; FILING DATE: 19-MAY-1993
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/944,882
;; FILING DATE: 10-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDonnell, John J
;; REGISTRATION NUMBER: 26,949
;; REFERENCE/DOCKET NUMBER: 93,510-D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; INFORMATION FOR SEQ ID NO: 39:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
;; US-08-389-926-39

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 13
US-08-578-686C-28
; Sequence 28, Application US/08578686C
; Patent No. 6028182
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; TITLE OF INVENTION: Methylphosphonic Acid Ester, Process For
; TITLE OF INVENTION: Preparing The Same And Its Use
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I. Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/578,686C
;; FILING DATE: January 2, 1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Johnson, Lori-Ann
;; REGISTRATION NUMBER: 34,498
;; REFERENCE/DOCKET NUMBER: 2481.1481-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-578-686C-28

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
|||||
Db 1 GATCAGCGTGCCTCAAA 18

RESULT 14
US-09-094-405-23
; Sequence 23, Application US/09094405
; Patent No. 6066720
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified oligonucleotides, their preparation
; TITLE OF INVENTION: and use
; NUMBER OF SEQUENCES: 30
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,405
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,196
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..18
; OTHER INFORMATION: /note= "PCNA (proliferating cell
; OTHER INFORMATION: nuclear antigen)"
; US-09-094-405-23

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctcctcaaa 18
| | | | | | | | | | | | | | | | | |
DB 1 GATCAGCGCTCCTCAAA 18

RESULT 15
US-09-144-112-28
; Sequence 28, Application US/09144112
; Patent No. 6150510
; GENERAL INFORMATION:
; APPLICANT: SEELA, Frank
; APPLICANT: THOMAS, Horst
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES, THEIR PREPARATION AND THEIR
; FILE REFERENCE: 026083/0181
; CURRENT APPLICATION NUMBER: US/09/144,112
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: DE P 44 38 918.3
; PRIOR FILING DATE: 1994-11-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antisense
; OTHER INFORMATION: Oligonucleotide
US-09-144-112-28

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctcctcaaa 18
| | | | | | | | | | | | | | | | | |
DB 1 GATCAGCGCTCCTCAAA 18

Search completed: October 12, 2002, 16:54:38
Job time: 8993 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 20:42:32 ; Search time 11685.9 Seconds
(without alignments)
33.325 Million cell updates/sec

Title: US-09-945-131-7

Perfect score: 18

Sequence: 1 gatcagcggtgctcaaa 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 10031574

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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- 2: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US080_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US081_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US082_COMB.seq.*
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- 22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq.*
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- 64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
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- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-07-944-882-22	Sequence 22, Appl
c 2	18	100.0	18	US-07-944-882-24	Sequence 24, Appl
3	18	100.0	18	US-07-995-022-20	Sequence 20, Appl
c 4	18	100.0	18	US-07-995-022-22	Sequence 22, Appl
5	18	100.0	18	US-08-110-294-17	Sequence 17, Appl
6	18	100.0	18	US-08-110-294-19	Sequence 19, Appl
c 7	18	100.0	18	US-08-110-294-38	Sequence 38, Appl
8	18	100.0	18	US-08-110-294-39	Sequence 39, Appl
9	18	100.0	18	US-08-240-106-22	Sequence 22, Appl
c 10	18	100.0	18	US-08-240-106-24	Sequence 24, Appl
11	18	100.0	18	US-08-386-577-2	Sequence 2, Appl
12	18	100.0	18	US-08-402-838-28	Sequence 28, Appl
13	18	100.0	18	US-08-463-012-2	Sequence 2, Appl
14	18	100.0	18	US-08-463-013-2	Sequence 2, Appl
15	18	100.0	18	US-08-463-014-2	Sequence 2, Appl
16	18	100.0	18	US-08-632-758-17	Sequence 17, Appl
c 17	18	100.0	18	US-08-632-758-19	Sequence 19, Appl
18	18	100.0	18	US-08-940-196-23	Sequence 23, Appl
19	18	100.0	18	US-09-241-561-7	Sequence 7, Appl
20	18	100.0	18	US-09-627-787-62	Sequence 62, Appl
21	18	100.0	18	US-09-643-233-28	Sequence 28, Appl
22	18	100.0	18	US-09-793-146-28	Sequence 28, Appl
23	18	100.0	18	US-09-835-370-51	Sequence 51, Appl
24	18	100.0	18	US-09-835-371-51	Sequence 51, Appl
c 25	15	83.3	30	US-07-944-882-19	Sequence 19, Appl
c 26	15	83.3	30	US-07-995-022-19	Sequence 19, Appl
c 27	15	83.3	30	US-08-240-106-21	Sequence 21, Appl
c 28	13.8	76.7	25	US-60-353-987-17512	Sequence 17512, A
29	13.8	76.7	25	US-60-353-987-169230	Sequence 169230, A
c 30	13.4	74.4	25	US-60-353-987-207077	Sequence 207077, A
c 31	13.4	74.4	30	US-08-110-294-15	Sequence 15, Appl

c 32 13.4 74.4 30 10 US-08-632-758-15 Sequence 15, Appl
c 33 13.4 74.4 37 29 US-09-746-375-21 Sequence 21, Appl
c 34 13.2 73.3 33 10 US-08-617-833-111 Sequence 111, Appl
c 35 13.2 73.3 33 10 US-08-617-833H-111 Sequence 111, Appl
c 36 13.2 73.3 34 13 US-08-950-860-10 Sequence 10, Appl
c 37 13.2 73.3 34 13 US-08-950-860B-10 Sequence 10, Appl
c 38 13.2 73.3 34 19 US-09-517-177-10 Sequence 10, Appl
c 39 13.2 73.3 39 4 US-08-064-385C-7 Sequence 7, Appl
c 40 13.2 73.3 39 4 US-08-064-385D-8 Sequence 8, Appl
c 41 13.2 73.3 39 8 US-08-465-292-7 Sequence 7, Appl
c 42 13.2 73.3 39 12 US-08-899-134-7 Sequence 7, Appl
c 43 13.2 73.3 39 30 US-09-781-811-22 Sequence 22, Appl
c 44 12.8 71.1 24 35 US-09-940-185-2835 Sequence 2835, Ap
c 45 12.8 71.1 25 35 US-09-954-427-84417 Sequence 84417, A

ALIGNMENTS

RESULT 1
US-07-944-882-22
; Sequence 22, Application US/07944882
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J.
; APPLICANT: Pratt, Richard
; APPLICANT: Gibbons, Gary
; TITLE OF INVENTION: INHIBITION OF PROLIFERATION OF VASCULAR
; TITLE OF INVENTION: SMOOTH MUSCLE CELL
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/944,882
FILING DATE: 19920910
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-56837/BIR;STAN-137
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 22:

LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-944-882-22

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGCGTGCCTCAAA 18

RESULT 2
US-07-944-882-24/c

; Sequence 24, Application US/07944882
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J.
; APPLICANT: Pratt, Richard
; APPLICANT: Gibbons, Gary
; TITLE OF INVENTION: INHIBITION OF PROLIFERATION OF VASCULAR
; TITLE OF INVENTION: SMOOTH MUSCLE CELL
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/944,882
FILING DATE: 19920910
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-56837/BIR;STAN-137
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 24:

LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-944-882-24

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatcaggcgtgcctcaaa 18
| | | | | | | | | | | | | | | | | |
Db 18 GATCAGCGTGCCTCAAA 1

RESULT 3

US-07-995-022-20
; Sequence 20, Application US/07995022
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J.
; TITLE OF INVENTION: Methods for in vivo delivery of
; TITLE OF INVENTION: therapeutic agents via HVJ-liposomes to cells of the
; TITLE OF INVENTION: vasculature
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegrretti & Witcoff, Ltd.
; STREET: Ten South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/995,022

; FILING DATE: 19921222
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,752
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; STRAIN: single
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /note= "ANTISENSE CYCLIN A +4 -
; OTHER INFORMATION: +21"
US-07-995-022-20

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGGCGTGCCTCAAA 18

RESULT 4
US-07-995-022-22/c
; Sequence 22, Application US/07995022
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Methods for in vivo delivery of
; TITLE OF INVENTION: therapeutic agents via HVJ-liposomes to cells of the
; TITLE OF INVENTION: vasculature
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: Ten South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL USA
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07995,022
; FILING DATE: 19921222
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,752
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs

; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..18
; OTHER INFORMATION: /note= "CONTROL SENSE CYCLIN A +4 -
; OTHER INFORMATION: +21"
US-07-995-022-22

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGGCGTGCCTCAAA 1

RESULT 5
US-08-110-294-17
; Sequence 17, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL USA
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-294-17

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18

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Db 1 GATCAGGCGTGCCTCAAA 18
|||||
RESULT 6
US-08-110-294-19/c
; Sequence 19, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-110-294-38

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
|||||
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 8
US-08-110-294-39
; Sequence 39, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-110-294-19

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
|||||
Db 18 GATCAGGCGTGCCTCAAA 1

RESULT 7
US-08-110-294-38/c
; Sequence 38, Application US/08110294
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; TITLE OF INVENTION: Inhibition of Proliferation of Vascular
; TITLE OF INVENTION: Smooth Muscle Cell
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Dr.
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,294
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,980
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/944,882
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,510-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-110-294-19
```

ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,510-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-110-294-39

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
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Db 1 GATCAGCGTGCCTCAAA 18

RESULT 9
US-08-240-106-22
Sequence 22, Application US/08240106
GENERAL INFORMATION:
APPLICANT: Dzau, Victor J
TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
TITLE OF INVENTION: THERAPEUTIC AGENTS VIA LIPOSOMES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,106
FILING DATE: 09-MAY-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-59079-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-240-106-22

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||

Db 1 GATCAGCGTGCCTCAAA 18

RESULT 10
US-08-240-106-24/c
Sequence 24, Application US/08240106
GENERAL INFORMATION:
APPLICANT: Dzau, Victor J
APPLICANT: Kaneda, Ysasufumi
TITLE OF INVENTION: METHOD FOR IN VIVO DELIVERY OF
TITLE OF INVENTION: THERAPEUTIC AGENTS VIA LIPOSOMES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,106
FILING DATE: 09-MAY-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-59079-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-240-106-24

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgtgcctcaaa 18
|||||

Db 18 GATCAGCGTGCCTCAAA 1

RESULT 11
US-08-386-577-2
Sequence 2, Application US/08386577
GENERAL INFORMATION:
APPLICANT: M le-Brune, Roxanne
APPLICANT: Proffit, Richard T.
TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOPLASMIC DELIVERY
TITLE OF INVENTION: OF AGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vestar, Inc.
STREET: 650 Cliffside Drive
CITY: San Dimas
STATE: California
COUNTRY: USA
ZIP: 91773

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cochran, Adam
; REGISTRATION NUMBER: 29,373
; REFERENCE/DOCKET NUMBER: D90
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (909)-394-4132
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-386-577-2

Query Match 100.0%; Score 18; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctgctcaaa 18
   |||||
DB 1 GATCAGCGCTGCCTCAA 18

RESULT 12
US-08-402-838-28
; Sequence 28, Application US/08402838
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; TITLE OF INVENTION: Polymide-Oligonucleotide Derivatives,
; TITLE OF INVENTION: Their Preparation And Use
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Warnement, Thalia V.
; REGISTRATION NUMBER: 39,064
; REFERENCE/DOCKET NUMBER: 02481.1437-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-402-838-28

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctgctcaaa 18
   |||||
DB 1 GATCAGCGCTGCCTCAA 18

RESULT 13
US-08-463-012-2
; Sequence 2, Application US/08463012
; GENERAL INFORMATION:
; APPLICANT: Proffit, Richard T.
; TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOPLASMIC DELIVERY
; TITLE OF INVENTION: OF AGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vestar, Inc.
; STREET: 650 Cliffside Drive
; CITY: San Dimas
; STATE: California
; COUNTRY: USA
; ZIP: 91773
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,012
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cochran, Adam
; REGISTRATION NUMBER: 29,373
; REFERENCE/DOCKET NUMBER: D90B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (909)-394-4132
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-463-012-2

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcgctgctcaaa 18
   |||||
DB 1 GATCAGCGCTGCCTCAA 18

RESULT 14
US-08-463-013-2
; Sequence 2, Application US/08463013
```


GENERAL INFORMATION:
APPLICANT: M le-Brune, Roxanne
TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOPLASMIC DELIVERY
TITLE OF INVENTION: OF AGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vestar, Inc.
STREET: 650 Cliffside Drive
CITY: San Dimas
STATE: California
COUNTRY: USA
ZIP: 91773
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,013
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cochran, Adam
REGISTRATION NUMBER: 29,373
REFERENCE/DOCKET NUMBER: D90A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (909)-394-4132
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-463-013-2

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
|||||
Db 1 GATCAGGCGGTGCTCAAA 18

RESULT 15
US-08-463-014-2
Sequence 2, Application US/08463014
GENERAL INFORMATION:
APPLICANT: M le-Brune, Roxanne
TITLE OF INVENTION: LIPID CONSTRUCTS FOR CYTOPLASMIC DELIVERY
TITLE OF INVENTION: OF AGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vestar, Inc.
STREET: 650 Cliffside Drive
CITY: San Dimas
STATE: California
COUNTRY: USA
ZIP: 91773
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,014
FILING DATE: 10-FEB-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cochran, Adam
REGISTRATION NUMBER: 29,373
REFERENCE/DOCKET NUMBER: D90C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (909)-394-4132
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-463-014-2

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcaggcggtgcctcaaa 18
|||||
Db 1 GATCAGGCGGTGCTCAAA 18

Search completed: October 12, 2002, 20:42:33
Job time: 16403 sec

2002